

FIGURE 1

CTAAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAATATTTAAATATT  
AATATACATTCTTCTGTCAGAAATACATAAAACTTATTATCAGCGCAGG  
5 GC GGCGCGGCGTCGGTCCCGGAGCAGAACCCGGCTTTCTGGAGCGACG  
CTGTCTCTAGTCGCTGATCCAAATGCACCGGCTCATCTTGTCTACACTCTA  
ATCTGCGCAAACCTTGAGCTGTCGGACACTTCTGCAACCCCGCAGAGCG  
CATCCATCAAAGCTTGCAGCAACGCCAACCTCAGGCAGATGAGAGCAATCA  
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG  
10 CTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTG  
ACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGTTGACA  
ATCAGTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTGT  
GGAAGTTGAAGATATATCCGAAACCAGTACCAATTAGAGGACGATGGTGT  
GGACACAAGGAAGTCCTCCAAGGATAAAATCAAGAACGAACCAAATTAAA  
15 ATCACATTCAAGTCCGATGACTACTTGTGGCTAACCTGGATTCAAGATTAA  
TTATTCTTGCTGGAAGATTCCAACCCGCAGCAGCTTCAGAGACCAACTGGG  
AACTGTCAAGCTCTATTCAAGGGTATCCTATAACTCTCCATCAGTAACG  
GATCCCACCTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAGAATTGATA  
CAGTGGAAAGATCTGCTCAAGTACTCAATCCAGAGTCATGGCAAGAAGATCT  
20 TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTACACCATGAC  
CGGAAGTCAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA  
GTTGCACTCCCAGGAATTACTCGGTCATATAAGAGAAGAGCTGAAGTTGGC  
CAATGTGGTCTTCTTCCACGTTGCCTCCTCGTCAGCGCTGTGGAGGAAATT  
GTGGCTGTGGAACTGTCAACTGGAGGTCTGCACATGCAATTCAAGGAAAAC  
25 CGTAAAAAGTATCATGAGGTATTACAGTTGAGCCTGGCCACATCAAGAGG  
AGGGGTAGAGCTAACGACCATGGCTCTAGTTGACATCCAGTTGGATACCATG  
AACGATGTGATTGTATCTGCAGCTCAAGACCACTCGATAAGAGAATGTGCA  
CATCCTTACATTAAGCCTGAAAGAACCTTAAAGGAGGGTGAGATAAG  
AGACCCCTTCTACCAGCAACCAAACCTACTACTAGCCTGCAATGCAATGAA  
30 CACAAGTGGTTGCTGAGTCTCAGCCTTGCTTGTAAATGCCATGGCAAGTAGA  
AAGGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCATTTAATAATA

GTGTTGAGGTATATGCACAAACACACAGAAATATTCATGTCTATG  
TGTATATAGATCAAATGTTTTGGTATATATAACCAGGTACACCAGAGCT  
TACATATGTTGAGTTAGACTCTAAAATCCTTGCCAAAATAAGGGATGGTC  
AAATATATGAAACATGTCTTAGAAAATTAGGAGATAAATTATTAAAT  
5 TTTGAAACACAAAACAATTGAAATCTGCTCTTAAAGAAAGCATCTTGTA  
TATTAAAATCAAAAGATGAGGCTTCTACATACATCTTAGTTG (SEQ ID  
NO:50)

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**FIGURE 2**

1 CTAaaaaatATGTTCTCTACAACACCAAGGCTCATTAAAATATT  
46 TAAATATTAATATACTACATTCTCTGTCAAGAAATACATAAAACTTT  
5 ATTATATCAGCGCAGGGCGCGCGCGTCGGTCCCAGGAGCAGAA  
136 CCCGGCTTTCTTGAGCGACGCTGTCTAGTCGCTGATCCCA  
181 AATGCACCGGCTCATCTTGCTACACTCTAAATCTGCGCAAACCT  
Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe  
10 226 TTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCAT  
Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile  
15 271 CAAAGCTTGGCGAACGCCAACCTCAGGCGAGATGAGAGCAATCA  
Lys Ala Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His  
316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGG  
Leu Thr Asp Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly  
20 361 AAACGGCTACGTGCAGAGTCCTAGATTCCGAACAGCTACCCAG  
Asn Gly Tyr Val Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg  
406 GAACCTGCTCCTGACATGGCGGTTCACTCTCAGGAGAATACACG  
Asn Leu Leu Leu Thr Trp Arg Leu His Ser Gln Glu Asn Thr Arg  
25 451 GATACAGCTAGTGTGACAATCAGTTGGATTAGAGGAAGCAGA  
Ile Gln Leu Val Phe Asp Asn Gln Phe Gly Leu Glu Glu Ala Glu  
496 AAATGATATCTGTAGGTATGATTTGTGGAAAGTTGAAGATATATC  
30 Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Asp Ile Ser  
541 CGAAACCAGTACCAATTATTAGAGGACGATGGGTGACACAAGGA  
Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly His Lys Glu  
35 586 AGTCCTCCAAGGATAAAATCAAGAACGAAACAAATTAAAATCAC  
Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys Ile Thr  
631 ATTCAAGTCCGATGACTACTTGTGGCTAACCTGGATTCAAGAT  
Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile  
40 676 TTATTATTCTTGCTGGAAGATTCCAACCCGAGCAGCTTCAGA  
Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ser Glu

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721 GACCAACTGGGAATCTGTACAGCTCTATTCAGGGGTATCCTA  
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr  
5 766 TAACTCTCCATCAGTAACGGATCCACTCTGATTGCGGATGCTCT  
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu  
811 GGACAAAAAAATTGCAGAATTGATACTGGAAAGATCTGCTCAA  
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys  
10 856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTA  
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr  
901 TCTGGACACCCCTCGGTATCGAGGCAGGTACCATGACCGGAA  
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys  
15 946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA  
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr  
20 991 CAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT  
SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu  
1036 GAAGTTGGCCAATGTGGCTTCTTCCACGTTGCCTCCTCGTGCA  
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln  
25 1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAACTGTCAACTGGAGGTC  
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer  
1126 CTGCACATGCAATTCAAGGGAAAACCGTGAAAAAGTATCATGAGGT  
CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal  
30 1171 ATTACAGTTGAGCCTGCCACATCAAGAGGAGGGGTAGAGCTAA  
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys  
35 1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG  
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys  
1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA  
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)  
40 1306 CATCCTTACATTAAGCCTGAAAGAACCTTGTAGTTAAGGAGGGTG  
1351 AGATAAGAGACCCTTTCTACCAGCAACCAAACCTACTACTAGC  
1396 CTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCT

1441 TTGTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACCTCTAT  
1486 ACCTAAGAATATAGGATTGCATTTATAATAGTGGTTGAGGTTAT  
1531 ATATGCACAAACACACACAGAAATATATTCTATGTCTATGTGTATA  
1576 TAGATCAAATGTTTTTGGTATATATAACCAGGTACACCAGAG  
5 1621 CTTACATATGTTGAGTTAGACTCTTAAATCCTTGCCAAAATA  
1666 AGGGATGGTCAAATATATGAAACATGTCTTAGAAAATTAGGAG  
1711 ATAAATTATTTAAATTGGAAACACAAAACAATTGAAATCT  
1756 TGCTCTCTAAAGAAAGCATCTGTATATTAAAAATCAAAAGATG  
1801 AGGCTTTCTTACATATACATCTTAGTTG (SEQ ID NO:50)

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20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

**FIGURE 3**

A -- Cur2 1.6 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTCAGAACCTATAACATGAAC  
TGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCATCCATTAGTA  
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTACCAT  
CTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA  
10 GCCGAGGACACGGCTGTATTACTGTGCGAGAGATATTATGATTACGTTG  
GGGAATTATCGCCTCGTTACTTGACTACTGGGCCAGGGAACCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

15 EVQLVESGGGLVKPGGLRLSCAASGFNFRTYNMNWRQAPGKGLEWVSSISSS  
SSNIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIAS  
FYFDYWGQGTLVTVSS (SEQ ID NO:13)

20 C -- Cur2 1.6 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCTGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TTTCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTGCCTAAAGTGGGGTCCCCTCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGAGTTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGCTCACITTCGGCGGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:56)

30 D -- Cur2 1.6 light chain amino acid sequence

35 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWFQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ  
ID NO:14)

**FIGURE 4**

A -- Cur2 1.11 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGGGAGGCTTGATCCAGCCTGGGGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGGTTACCGTCAGTAGCAACTACATGAGC  
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTATA  
GCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTC  
CAGAGACAATTCCAAGAACACGCTGTATCTCAAATGAACAGCCTGAGAGCC  
10 GAGGACACGGCCGTGTATTACTGTGCGGGAACGGTGAACAGAATTACTACT  
ACGGTATGGACGTCTGGGCCAACGGACCACGGTACCGTCTCCTCAG (SEQ  
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

15 EVQLVQSGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG  
GSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTNYYGM  
DVWGQGTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

20 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCAAAGTAATGGATAC  
AACTATTGGATTGGTACCTGCAGAACGCCAGGGCAGTCTCACAGCTCCTGA  
TCTATTGGGTTCTAATCGGGCCTCCGGGTCCTGACAGGTTAGTGGCAGT  
GGATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG  
25 TTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCTCACTTCGGCGGAGGG  
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

30 DIVMTQSPLSLPVTPGEPASISCRSSQSLLQSNGNYLDWYLQKPGQSPQLLIYLG  
SNRASGVPDFRSGSGSTDFTLKISRVEAEDVGYYCMQALQTLTFGGGKVEI  
K (SEQ ID NO:16)

**FIGURE 5**

A -- Cur2 1.17 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGAGGCCTGGTCCAGCCTGGGAAGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC  
10 TGGTCCGCCAGGCTCCAGGAAGGGCTGGAGTGGGTGGCAGTTATATGGT  
ATGATGGAAGTAATAAAACTATGCAGACTCCGTGAAGGGCCGATTACCAT  
15 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTGTATTACTGTGCAGAGATCAAGGATAACAGATATG  
CTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:59)

15 B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW  
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYA  
20 GYYDYGMDVWGQGTTVTVSS (SEQ ID NO:17)

25 C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
25 GTTGCAAAGTGGGTCCCCTCAAGGTTAGCGGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGCTCACTTCGGCGGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:60)

30 D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGTKVEIK (SEQ  
35 ID NO:18)

**FIGURE 6**

A -- Cur2 1.18 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCAAACAGTGGTAAACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC  
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC  
TGGGACATACTACTACTACGGTATGGACGTCTGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:61)

15 B -- Cur2 1.18 heavy chain protein sequence

20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAG  
YYYYYYGMDVWGQGTTTVSS (SEQ D NO:19)

25 C -- Cur2 1.18 light chain nucleotide sequence

30 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTCT  
GTCTACAGCATAATAGTTACCCATTCACTTCGGCCCTGGGACCAAAGTGGAT  
ATCAAAC (SEQ ID NO:62)

35 D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ  
ID NO:20)

**FIGURE 7**

A -- Cur2 1.19 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCGTTATGATATCAAC  
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAAC  
CCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCA  
TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG  
10 ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTG  
GGGGAGTTATCGTGCACACGGTATGGACGTCTGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFG  
GVIVHYGMDVWGQGTTVTVSS (SEQ ID NO:21)

20 C -- Cur2 1.19 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCTGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTGCAAAGTGGGGTCCCCTCAAGGTTAGCGGGCAGTGGATCTGGGACAGA  
TTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTGACCCGTGCAGTTGGCCAGGGACCAAGCTGGA  
GATCAGAC (SEQ ID NO:64)

30 D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTDFLTISLQPEDFATYYCLQHNSDPCSFGQGTKLEIR (SEQ  
ID NO:22)

35

**FIGURE 8**

A -- Cur2 1.23 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCGGGGAGTCT  
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTACCAAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTGACTCTGATACCAGATAACAGCCGCTTCCAAGGCCAGGTACCA  
10 TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GCCCTCGGACACCGCCATGTATTACTGTGCGAGACATGTATCGTATTACTATG  
TTTCGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGAAACCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

15 EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCARHVSYYYVSGS  
YYNVFDYWQGTLTVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGATACCAGGGAAAGCCCTAACGCCTGATCTATGCTGCATCCA  
GTTTGCAACGTGGGGTCCCCTCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
25 GTCTACAGCATAATAGTTACCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

30 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR  
GVPSRFGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:24)

**FIGURE 9**

A -- Cur2 1.24.1 heavy chain nucleotide sequence

5

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTCACTAGTTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCAGATATATGGT  
ATGATGGAAGTAATAAAATACTATGCAGACTCCGTGAAGGGCCGATTCAACCAT  
10 CTCCAGAGACAATTCCAAGAACACCGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTATTATTGTGCGAGAGATCAGGGATAACAGCTATG  
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCCTCTCCTCAG (SEQ ID NO:67)

15 B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGVVQPGRLRLSCAASGFSFSSYGMHWVRQAPGKGLEWWADIW  
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYSYG  
YVYYDYGMDVWGQGTTVTVSS (SEQ ID NO:25)

20

C -- Cur2 1.24.1 light chain nucleotide sequence

25

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTCAAAGTGGGGTCCCCTCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  
GTTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:68)

30

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYASSLQ  
SGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGQTKVEIK (SEQ

35

ID NO:26)

**FIGURE 10**

A -- Cur2 1.25.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCAGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTCTGGATACAGGTTACCACTGGATCGG  
CTGGGTGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTACTCTGATACCAAGATAACAGCCCCTACCTGCAGTGGAGCAGCCTGAA  
10 TCTCAGCCACAAGTCCATCAGCACCGCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG  
GTTCGGAGACTTATTATAATGTCTTGACTACTGGGCCAGGGAACCCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKIISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYYGSET  
YYNVFDYWGQGTLTVSS (SEQ ID NO:27)

20 C -- Cur2 1.25.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTGCAAAGTGGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:70)

30 D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGQGTKVEIK (SEQ  
ID NO:28)

35

**FIGURE 11**

## A -- Cur2 1.29 heavy chain nucleotide sequence

5 GAGGTGCA GCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGAGTCT  
CTGAAGATCTCCTGTAAAGGGTCTGGATACAGCTTACCAAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTGA CTCGTATACCAAGATACAGCCGTCCTCCAAGGCCAGGCCACCA  
10 TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGGCT  
ACGATTGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGGCCAAG  
GGACCACGGTCACCGTCTCCTCAG (SEQ ID NO:71)

## B -- Cur2 1.29 heavy chain protein sequence

15 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMYCARHVDVGATIGG  
YYYYYHGMDVWGOGTTVTVSS (SEQ ID NO:29)

20 C -- Cur2 1.29 light chain nucleotide sequence

25 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC  
GCCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA  
ACTATTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAACCTCCTGATC  
TATTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTAGTGGCAGTGG  
ATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT  
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCTCATGTGCAGTTGGCCA  
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

30 D -- Cur2 1.29 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLIYLG  
SNRASGVPDFRSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKL  
EIK (SEQ ID NO:30)

35

**FIGURE 12**

A -- Cur2 1.33 heavy chain nucleotide sequence

5 CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCACTATGGTATCAGC  
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG  
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG  
10 ATCTGACGACACGGCCGTGTATTACTGTGCCAGAGAGATCATTACTATGATAGT  
AGTGATTATCTCTACTACTACCGTTGGACGTCTGGGCCAAGGGACCAC  
GGTCACCGTCTCCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYYDSS  
DYLYYYYGLDVWGQGTTVTVSS (SEQ ID NO:31)

20 C -- Cur2 1.33 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT  
ATCAGCAGAAACCAGGGAAAGTTCTTAAGCTCCTGATCTATGCTGCATCCAC  
TTTGCAATCAGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGACAGATT  
TCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT  
CAAAAGTATAACAGTGCCCCGCTACTTCGGCGGAGGGACCAAGGTGGAGA  
TCAAAC (SEQ ID NO:74)

30 D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQ  
SGVPSRFSGSGSGTDFLTISLQPEDVATYYCQKYNSAPLTFGGGTKEIK (SEQ  
ID NO:32)

35

**FIGURE 13**

A -- Cur2 1.38.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAATTATATGGT  
ATGATGGAAATGATAAATACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT  
10 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTATTACTGTGCAGAGAGGATATTACTATGATAGTA  
GTGATTATCTCTACTACTACGGTATGGACGTCTGGGCCAAGGGACCAC  
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

15 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWIY  
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS  
DYLYYYYGMDVWGQGTTVTVSS (SEQ ID NO:33)

20 C -- Cur2 1.38.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGT  
ATCAGCAGAAACCAAGGGAAAGTTCTAACCTCCTGATCTATGCTGCATCCAC  
TTTGCAATCAGGGTCCCCTCGGTTAGTGGCAGTGGATCTGGACAGATT  
TCTCTCTACCACATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT  
CAAAGTGTAAACAGTGCCCGTGGACGTTGGCCAAGGGACCACGGTGGAG  
ATCAAAC (SEQ ID NO:76)

30 D -- Cur2 1.38.1 light chain protein sequence

35 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASTLQ  
SGVPSRFSGSGSGTDFSLTISSLQPEDVAAYYCQKCNSAPWTFQGQGTTVEIK (SEQ  
ID NO:34)

**FIGURE 14**

A -- Cur2 1.39.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGAACAGAGGTGAAAAAGCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGTTCTGGATACAGGTTACCAAGCTACTGGATCGG  
CTGGTGCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTACTCTGATACAGATAACAGCCCCTACCTGCAGTGGAGCAGCCTGAA  
10 TCTCAGCCACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA  
ATTCGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGGAACCCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

15 EVQLVQSGTEVKKPGESELKISCKGSYRFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYYNSGS  
YYNVFDYWGQGTLTVSS (SEQ ID NO:35)

20 C -- Cur2 1.39.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTGCAAAGTGGGTCCCATCAAGGTTAGCAGCGGAGTGGATCTGGACAGA  
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:78)

30 D -- Cur2 1.39.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:36)

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**FIGURE 15**

A -- Cur2 1.40.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTTACCACTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAGTGGTAACACACAGGCTATGCACAGAACGTTCCAGGGCAGAGTCACC  
10 ATGACCAGGAACACACCTCCCTAACGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT  
AGCTGCTACCAACTACTACAACGGTATGGACGTCTGGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDTAVYYCARDIVVVV  
AATNYYNGMDVWGQGTTVTVSS (SEQ ID NO:37)

20

ABX-Cur2 pat app.1

**FIGURE 16**

A -- Cur2 1.45 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTTCACCAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAGTGGTAACACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC  
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA  
TGGTTACGACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTC  
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG  
YDYYYGMDVWGQGTTVTVSS (SEQ ID NO:38)

20 C -- Cur2 1.45 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCAATTGCCGGCGAGTCAGGGCATTAGCAATGATTAGCCTGG  
TATCAGCAGAAACCAGGGAAAGTTCTTAAGCTCCTGATCTATGCTGCATCCA  
CTTGCAATTAGGGTCCCATCTGGTCAGTGGCAGTGGATCTGGACAGAT  
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG  
TCAAAAGTATAACAGTCCCCATTCACTTCCGGCCCTGGACCAAAGTGGAT  
ATCAAAC (SEQ ID NO:81)

30 D -- Cur2 1.45 light chain protein sequence

35 DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQ  
LGVPSRFSGSQGTDFTLTISLQPEDVATYYCQKYNsapFTFGPGTKVDIK (SEQ  
ID NO:39)

200 150 100 50 0

**FIGURE 17**

A -- Cur2 1.46.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACTCCTTACCAAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAAATGGTAACACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC  
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT  
AACTGCTACGGACTACTACGGTATGGACGTCTGGGCCAAGGGACCAACG  
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGY SFTSYDINWVRQATGQGLEWMGWM  
NPNNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVT  
ATDYYYGMDVWGQGTTTVSS (SEQ ID NO:40)

20 C -- Cur2 1.46.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATTCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCTAACGCCTGATTTGCTGCATCCA  
GTTTGCCAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT  
GTCTACAGCATAGTGGTACCCCTCCGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:83)

30 D -- Cur2 1.46.1 light chain protein sequence

35 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLPS  
GVPSRFSGSGTEFTLTISLQPEDFATYYCLQHSGYPPFGQGTKVEIK (SEQ ID  
NO:41)

ABX-Cur2 pat app.1

**FIGURE 18**

A -- Cur2 1.48.1 heavy chain nucleotide sequence

5 CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGTACACCTTACCAAGCTATGGTATCAGC  
TGGGTGCACAGGCCCTGGACAAGGGCTGAGTGGATGGATGGATCAGCG  
CTTACAATGGTAACACAAACTATGCACAGAACGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG  
10 ATCTGACGACACGGCCGTATTACTGTGCGAGAGATGTTGAATATTACTATG  
ATGGTAGTGGTTATTACTACTTTGACTACTGGGCCAGGAAACCCTGGTCACC  
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCARDVEYYD  
GSGYYYFDYWQGQTLTVVSS (SEQ ID NO:42)

20 C -- Cur2 1.48.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCTCCGTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGTGGCGAGTCAGGGTATTAGCAGCTGGTAGCCTGG  
TATCAGCAGAAACCAGGGAAAGGCCCTAACGGTTAGCAGCGCAGTGGATCTGGGACAGA  
TTTGCAAAGTGGGGTCCCATTCAAGGTTAGCAGCGCAGTGGATCTGGGACAGA  
TTTCACTCTCACCACAGCAGCCTGCAGCCTGAGGATTTGCATCTTACTATT  
GTCAACAGTCTAACAGTTCCCTCGGACGTTCGGCCAAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:85)

30 D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRVITCRASQGISSWLAWYQQKPGKAPKLLIYAASILQ  
SGVPSRFSGSGTDFLTISLQPEDFASYYCQQNSFPRTFGQGTKVEIK (SEQ  
ID NO:43)

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**FIGURE 19**

A -- Cur2 1.49.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCAAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAGTGGTACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC  
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTTCTGTGCGAGAAATGAGGGATATACTGGC  
TACGAGCTATTACTACTACTTACGGTATGGACGTCTGGGCCAAGGGACC  
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

15 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATQGLEWMGWM  
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDIVAT  
SYYYYFYGMDVWGQGTTVTVSS (SEQ ID NO:44)

20 C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA  
ACTATTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC  
25 TATTGGGTCTAGTCGGGCCTCCGGGTCCTGACAGGTTAGTGGCAGTGG  
ATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT  
GGGGTTATTACTGCATGCAAACACTACAAACTATCACCTCGGCCAAGGGA  
CACGACTGGAGATTAAAC (SEQ ID NO:87)

30 D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGYNLDWYLLKPGQSPQLLIYLG  
SSRASGVPDFRFSGSQTDFTLKISRVEAEDVGVYYCMQTLQITFGQGTRLEIK  
(SEQ ID NO:45)

35

**FIGURE 20**

A -- Cur2 1.51 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGAGCTGAGGTGAAAAAGCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGTTCTGGATACAGCTTACCAAGCTACTGGATCGG  
CTGGGTGCCAGATGCCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTACTCTGATGCCAAATACAGCCGCTACCTGCAGTGGAGCAGCCTGAA  
10 TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTGGAA  
GGAATTATCGGTATACAGGGTGGTTCGACCCCTGGGGCCAGGGAACCTGGT  
CACCGTCTCCTCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKI<sup>S</sup>CKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPG  
DSDAKYSPSFQGQVTISADKSISTA<sup>L</sup>QWSSLKASDTAMYYCARHYDYVWRNY  
RYTGWFDPWGQGTLTVSS (SEQ ID NO:46)

20 C -- Cur2 1.51.1 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCGTCTTGTCTCCAGGGGAAAG  
AGCCACCCTCTCCTGCA<sup>G</sup>GGCCAGTCAGAGTGT<sup>T</sup>AGCAGCAGCTACTTAGCC  
TGGTACCAGCAGAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCAT  
25 CCAACAGGGCCACTGGCATCCCAGACAGGTTCA<sup>G</sup>TGGCAGTGGTCTGGAC  
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATT  
ACTGTCAGCAGTATGGTAGCTCACTATTCACTT<sup>C</sup>GGCCCTGGACCAAAAGTG  
GATATCAAAC (SEQ ID NO:89)

30 D -- Cur2 1.51.1 light chain protein sequence

EIVLTQSPGTL<sup>S</sup>LSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA  
TGIPDRFSGSGSGTDF<sup>L</sup>TISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK (SEQ  
ID NO:47)

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**FIGURE 21**

A -- Cur2 6.4 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTCTGGATACACCTTCACCAGTTATGATATCAAC  
10 TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATAAAC  
CCTAATAGTGGTAACACAGACTATGCACAGAAGTCCAGGGCAGAGTCACCA  
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG  
ATCTGAGGACACGCCATATATTATTGTGTGAGAGGCTTGGATACAGCTAT  
15 AATTACGACTACTATTACGGTATGGACGTCTGGGCAAGGGACCACGGTCA  
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN  
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY  
DYYYGMDVWGQQGTTVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

20 GAAATTGTGTTGACGCAGTCTCCAGGCACCCGTCTTGTCTCCAGGGAAAG  
AGCCACCCCTCTCCTGCAGGCCAGTCAGAGTGTAGTAGTTACTTAGCCT  
GGTACCAGCAGAACGCTGCCAGGCTCCAGGCTCTCATCTATGCTACATC  
CAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGTCTGGGACA  
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATTA  
25 CTGTCAGCAGTATGGTAGTTCACCGTGCAGTTGGCCAGGGGACCAAGCTG  
GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

30 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA  
TGIPDRFSGSGSGTDFLTISLEPEDFAVYYCQQYGSSPCSFQGQTKLEIK (SEQ  
ID NO:49)

**FIGURE 22A**

| Clone  | Germline genes used |       |       | No. of Nucleotide/ Amino acid changes |     |      |     |      |       |      |     |
|--------|---------------------|-------|-------|---------------------------------------|-----|------|-----|------|-------|------|-----|
|        |                     | V     | D     | J                                     | FR1 | CDR1 | FR2 | CDR2 | FR3   | CDR3 | FR4 |
| CR2    |                     | V     | D     | J                                     | V   |      |     |      | D & J |      |     |
| 1.19.1 | VH                  | V1-8  | D3-16 | JH6B                                  | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK2                                   | 0/0 | 0/0  | 0/0 | 0/0  | 1/1   | 1/1  | 0/0 |
| 6.4.1  | VH                  | V1-8  | D5-18 | JH6B                                  | 0/0 | 0/0  | 0/0 | 3/2  | 5/3   | 0/0  | 0/0 |
|        | VK                  | A27   |       | JK2                                   | 0/0 | 3/0  | 1/0 | 2/2  | 0/0   | 1/0  | 0/0 |
| 1.18   | VH                  | V1-8  | D6-19 | JH6B                                  | 1/0 | 0/0  | 0/0 | 1/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK3                                   | 0/0 | 0/0  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
| 1.40.1 | VH                  | V1-8  | D2    | JH6B                                  | 1/0 | 1/1  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
|        | VK                  | mix   |       |                                       |     |      |     |      |       |      |     |
| 1.45   | VH                  | V1-8  | DK4   | JH6B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A20   |       | JK3                                   | 1/1 | 1/1  | 0/0 | 1/1  | 0/0   | 0/0  | 0/0 |
| 1.46.1 | VH                  | V1-8  | D2    | JH6B                                  | 1/0 | 1/1  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 2/1 | 1/1  | 0/0   | 2/2  | 0/0 |
| 1.49.1 | VH                  | V1-8  | D5-12 | JH6B                                  | 1/0 | 0/0  | 0/0 | 1/1  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A19   |       | JK5                                   | 0/0 | 0/0  | 1/1 | 1/1  | 0/0   | 1/1  | 0/0 |
| 1.33   | VH                  | V1-18 | D21-9 | JH6B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A20   |       | JK4                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.48.1 | VH                  | V1-18 | D21-9 | JH4B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | L5    |       | JK1                                   | 0/0 | 0/0  | 0/0 | 1/1  | 2/1   | 1/1  | 0/0 |
| 1.6.1  | VH                  | V3-21 | D3-16 | JH4B                                  | 0/0 | 4/4  | 0/0 | 1/1  | 1/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK4                                   | 0/0 | 0/0  | 1/1 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.17.1 | VH                  | V3-33 | D5-18 | JH6B                                  | 2/1 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK4                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.24.1 | VH                  | V3-33 | D5-18 | JH6B                                  | 0/0 | 2/1  | 0/0 | 1/1  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 0/0 | 0/0  | 1/0   | 0/0  | 0/0 |
| 1.38.1 | VH                  | V3-33 | D21-9 | JH6B                                  | 1/0 | 0/0  | 0/0 | 3/3  | 2/1   | 0/0  | 0/0 |
|        | VK                  | A20   |       | JK1                                   | 0/0 | 0/0  | 1/1 | 0/0  | 2/2   | 1/1  | 0/0 |
| 1.11.1 | VH                  | V3-53 | D4-17 | JH6B                                  | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A19   |       | JK4                                   | 0/0 | 1/1  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.23.1 | VH                  | V5-51 | D3-10 | JH4B                                  | 1/1 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 1/1 | 1/1  | 0/0   | 0/0  | 0/0 |
| 1.25.1 | VH                  | V5-51 | D3-10 | JH4B                                  | 1/0 | 1/1  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.29   | VH                  | V5-51 | D5-12 | JH6B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A19   |       | JK2                                   | 0/0 | 0/0  | 1/0 | 0/0  | 1/1   | 0/0  | 0/0 |
| 1.39.1 | VH                  | V5-51 | D3-10 | JH4B                                  | 2/1 | 1/1  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.51.1 | VH                  | 5-51  | D3-16 | JH5B                                  | 2/0 | 0/0  | 0/0 | 1/1  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A27   |       | JK3                                   | 0/0 | 0/0  | 0/0 | 1/1  | 0/0   | 0/0  | 0/0 |

**FIGURE 22B**

| Clone  | Germline genes used |       |       | No. of Nucleotide/ Amino acid changes |     |      |     |      |       |      |     |
|--------|---------------------|-------|-------|---------------------------------------|-----|------|-----|------|-------|------|-----|
|        |                     | V     | D     | J                                     | FR1 | CDR1 | FR2 | CDR2 | FR3   | CDR3 | FR4 |
| CR2    |                     | V     | D     | J                                     | V   |      |     |      | D & J |      |     |
| 1.40.1 | VH                  | V1-8  | D2    | JH6B                                  | 1/0 | 1/1  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
|        | VK                  | mix   |       |                                       |     |      |     |      |       |      |     |
| 1.48.1 | VH                  | V1-18 | D21-9 | JH4B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | L5    |       | JK1                                   | 0/0 | 0/0  | 0/0 | 1/1  | 2/1   | 1/1  | 0/0 |
| 1.49.1 | VH                  | V1-8  | D5-12 | JH6B                                  | 1/0 | 0/0  | 0/0 | 1/1  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A19   |       | JK5                                   | 0/0 | 0/0  | 1/1 | 1/1  | 0/0   | 1/1  | 0/0 |
| 1.11.1 | VH                  | V3-53 | D4-17 | JH6B                                  | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A19   |       | JK4                                   | 0/0 | 1/1  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.29   | VH                  | V5-51 | D5-12 | JH6B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A19   |       | JK2                                   | 0/0 | 0/0  | 1/0 | 0/0  | 1/1   | 0/0  | 0/0 |
| 1.45   | VH                  | V1-8  | DK4   | JH6B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A20   |       | JK3                                   | 1/1 | 1/1  | 0/0 | 1/1  | 0/0   | 0/0  | 0/0 |
| 1.33   | VH                  | V1-18 | D21-9 | JH6B                                  | 1/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A20   |       | JK4                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.38.1 | VH                  | V3-33 | D21-9 | JH6B                                  | 1/0 | 0/0  | 0/0 | 3/3  | 2/1   | 0/0  | 0/0 |
|        | VK                  | A20   |       | JK1                                   | 0/0 | 0/0  | 1/1 | 0/0  | 2/2   | 1/1  | 0/0 |
| 6.4.1  | VH                  | V1-8  | D5-18 | JH6B                                  | 0/0 | 0/0  | 0/0 | 3/2  | 5/3   | 0/0  | 0/0 |
|        | VK                  | A27   |       | JK2                                   | 0/0 | 3/0  | 1/0 | 2/2  | 0/0   | 1/0  | 0/0 |
| 1.51.1 | VH                  | 5-51  | D3-16 | JH5B                                  | 2/0 | 0/0  | 0/0 | 1/1  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A27   |       | JK3                                   | 0/0 | 0/0  | 0/0 | 1/1  | 0/0   | 0/0  | 0/0 |
| 1.19.1 | VH                  | V1-8  | D3-16 | JH6B                                  | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK2                                   | 0/0 | 0/0  | 0/0 | 0/0  | 1/1   | 1/1  | 0/0 |
| 1.18   | VH                  | V1-8  | D6-19 | JH6B                                  | 1/0 | 0/0  | 0/0 | 1/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK3                                   | 0/0 | 0/0  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
| 1.6.1  | VH                  | V3-21 | D3-16 | JH4B                                  | 0/0 | 4/4  | 0/0 | 1/1  | 1/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK4                                   | 0/0 | 0/0  | 1/1 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.23.1 | VH                  | V5-51 | D3-10 | JH4B                                  | 1/1 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 1/1 | 1/1  | 0/0   | 0/0  | 0/0 |
| 1.25.1 | VH                  | V5-51 | D3-10 | JH4B                                  | 1/0 | 1/1  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.39.1 | VH                  | V5-51 | D3-10 | JH4B                                  | 2/1 | 1/1  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.17.1 | VH                  | V3-33 | D5-18 | JH6B                                  | 2/1 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK4                                   | 0/0 | 0/0  | 0/0 | 0/0  | 0/0   | 0/0  | 0/0 |
| 1.24.1 | VH                  | V3-33 | D5-18 | JH6B                                  | 0/0 | 2/1  | 0/0 | 1/1  | 0/0   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 0/0 | 0/0  | 1/0   | 0/0  | 0/0 |
| 1.46.1 | VH                  | V1-8  | D2    | JH6B                                  | 1/0 | 1/1  | 0/0 | 0/0  | 1/1   | 0/0  | 0/0 |
|        | VK                  | A30   |       | JK1                                   | 0/0 | 0/0  | 2/1 | 1/1  | 0/0   | 2/2  | 0/0 |

**FIGURE 23**

**Figure 23A**

|               |       |   |                         |     |    |    |     |  |  |  | Section 1 |
|---------------|-------|---|-------------------------|-----|----|----|-----|--|--|--|-----------|
|               | (1)   | 1   | 10                      | 20  | 30 | 40 | 51  |  |  |  |           |
| CUR2-1.6.1_HC | (1)   | EVQLVESGGGLVKPGGSLRLSCAASGPNFR                      | TYNMNWVRQAPGKGLEWVSSI   |     |    |    |     |  |  |  |           |
| VH3-21        | (1)   | EVQLVESGGGLVKPGGSLRLSCAASGFTFSS                     | SYSMNWVRQAPGKGLEWVSSI   |     |    |    |     |  |  |  |           |
| Consensus     | (1)   | EVQLVESGGGLVKPGGSLRLSCAASGF                         | F SY MNWVRQAPGKGLEWVSSI |     |    |    |     |  |  |  |           |
|               |       |   |                         |     |    |    |     |  |  |  | Section 2 |
|               | (52)  | 52  | 60                      | 70  | 80 | 90 | 102 |  |  |  |           |
| CUR2-1.6.1_HC | (52)  | SSSSSNIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMI |                         |     |    |    |     |  |  |  |           |
| VH3-21        | (52)  | SSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR     | ---                     |     |    |    |     |  |  |  |           |
| Consensus     | (52)  | SSSSS IYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR     |                         |     |    |    |     |  |  |  |           |
|               |       |   |                         |     |    |    |     |  |  |  | Section 3 |
|               | (103) | 103   | 110                     | 126 |    |    |     |  |  |  |           |
| CUR2-1.6.1_HC | (103) | TFGGIIASFYFDYWGQGTIVTVSS                            |                         |     |    |    |     |  |  |  |           |
| VH3-21        | (99)  | -----   |                         |     |    |    |     |  |  |  |           |
| Consensus     | (103) |   |                         |     |    |    |     |  |  |  |           |

5

**Figure 23B**

|               |       |                                     |                 |                |    |    |     |  |  |  | Section 1 |
|---------------|-------|-------------------------------------|-----------------|----------------|----|----|-----|--|--|--|-----------|
|               | (1)   | 1                                   | 10              | 20             | 30 | 40 | 51  |  |  |  |           |
| CUR2-1.6.1_LC | (1)   | DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGW | F QQKPGKAPKR    | LIYAA          |    |    |     |  |  |  |           |
| A30           | (1)   | DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGW | Y QQKPGKAPKR    | LIYAA          |    |    |     |  |  |  |           |
| Consensus     | (1)   | DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGW | F QQKPGKAPKR    | LIYAA          |    |    |     |  |  |  |           |
|               |       |                                     |                 |                |    |    |     |  |  |  | Section 2 |
|               | (52)  | 52                                  | 60              | 70             | 80 | 90 | 102 |  |  |  |           |
| CUR2-1.6.1_LC | (52)  | SSLQSGVPSRFSGSG8GTEFTLT             | TISSLQPEDFATYYC | LQHNSYPLTFGGGT |    |    |     |  |  |  |           |
| A30           | (52)  | SSLQSGVPSRFSGSG8GTEFTLT             | TISSLQPEDFATYYC | LQHNSYPLTFGGGT |    |    |     |  |  |  |           |
| Consensus     | (52)  | SSLQSGVPSRFSGSG8GTEFTLT             | TISSLQPEDFATYYC | LQHNSYPLTFGGGT |    |    |     |  |  |  |           |
|               |       |                                     |                 |                |    |    |     |  |  |  | Section 3 |
|               | (103) | 103                                 | 107             |                |    |    |     |  |  |  |           |
| CUR2-1.6.1_LC | (103) | KVEIK                               |                 |                |    |    |     |  |  |  |           |
| A30           | (96)  | -----                               |                 |                |    |    |     |  |  |  |           |
| Consensus     | (103) |                                     |                 |                |    |    |     |  |  |  |           |

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**FIGURE 24**

**Figure 24A**

|                |   |     |     |    |    | Section 1 |
|----------------|---|-----|-----|----|----|-----------|
|                | (1) 1   | 10  | 20  | 30 | 40 | 51        |
| Cur2-1.11.1 HC | (1) EVQLVESGGGLIOPGGSLRLSCAASGFTVSSNYM3WVRQAPGKGLEWVSVI |     |     |    |    |           |
| VH3-53         | (1) EVQLVESGGGLIOPGGSLRLSCAASGFTVSSNYM3WVRQAPGKGLEWVSVI |     |     |    |    |           |
| Consensus      | (1) EVQLVESGGGLIOPGGSLRLSCAASGFTVSSNYM3WVRQAPGKGLEWVSVI |     |     |    |    |           |
|                |   |     |     |    |    | Section 2 |
|                | (2) 52  | 60  | 70  | 80 | 90 | 102       |
| Cur2-1.11.1 HC | (2) YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN |     |     |    |    |           |
| VH3-53         | (2) YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----- |     |     |    |    |           |
| Consensus      | (2) YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA       |     |     |    |    |           |
|                |   |     |     |    |    | Section 3 |
|                | (103) 103   | 110 | 120 |    |    |           |
| Cur2-1.11.1 HC | (103) YYYGMDVWGQGTTVTVSS                                |     |     |    |    |           |
| VH3-53         | (98) -----  |     |     |    |    |           |
| Consensus      | (103)   |     |     |    |    |           |

5

**Figure 24B**

|                |   |     |    |    |    | Section 1 |
|----------------|---|-----|----|----|----|-----------|
|                | (1) 1   | 10  | 20 | 30 | 40 | 51        |
| CUR2-1.11.1_LC | (1) DIVMTQSPLSLPVTPGEPASISCRSSSQSLLQSNGNYLDWYLQKPGQSPQL |     |    |    |    |           |
| A19            | (1) DIVMTQSPLSLPVTPGEPASISCRSSSQSLLH3NGNYLDWYLQKPGQSPQL |     |    |    |    |           |
| Consensus      | (1) DIVMTQSPLSLPVTPGEPASISCRSSSQSLL SNGNYLDWYLQKPGQSPQL |     |    |    |    |           |
|                |   |     |    |    |    | Section 2 |
|                | (2) 52  | 60  | 70 | 80 | 90 | 102       |
| CUR2-1.11.1_LC | (2) LIYLGSRASGVEDRFGSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF |     |    |    |    |           |
| A19            | (2) LIYLGSRASGVEDRFGSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP-- |     |    |    |    |           |
| Consensus      | (2) LIYLGSRASGVEDRFGSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP   |     |    |    |    |           |
|                |   |     |    |    |    | Section 3 |
|                | (103) 103   | 111 |    |    |    |           |
| CUR2-1.11.1_LC | (103) GGGTKVEIK   |     |    |    |    |           |
| A19            | (101) -----   |     |    |    |    |           |
| Consensus      | (103)   |     |    |    |    |           |

**FIGURE 25**

**Figure 25A**

|               |       |   |                                   |     |    |    | Section 1 |
|---------------|-------|---|-----------------------------------|-----|----|----|-----------|
|               | (1)   | 10  | 20                                | 30  | 40 | 51 |           |
| CR2-1.17.1_HC | (1)   | QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVI |                                   |     |    |    |           |
| VH3-33        | (1)   | QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVI |                                   |     |    |    |           |
| Consensus     | (1)   | QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVI |                                   |     |    |    |           |
|               |       |   |                                   |     |    |    | Section 2 |
|               | (52)  | 52  | 60                                | 70  | 80 | 90 | 102       |
| CR2-1.17.1_HC | (52)  | WYDGSNKKYYADSVKGRFTI                                | SRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY |     |    |    |           |
| VH3-33        | (52)  | WYDGSNKKYYADSVKGRFTI                                | SRDN SKNTLYLQMNSLRAEDTAVYYCAR     | --- |    |    |           |
| Consensus     | (52)  | WYDGSNKKYYADSVKGRFTI                                | SRDN SKNTLYLQMNSLRAEDTAVYYCAR     |     |    |    |           |
|               |       |   |                                   |     |    |    | Section 3 |
|               | (103) | 103   | 110                               | 126 |    |    |           |
| CR2-1.17.1_HC | (103) | RYAGYYYYDYGMDVWGQGTTTVSS                            |                                   |     |    |    |           |
| VH3-33        | (99)  | -----   |                                   |     |    |    |           |
| Consensus     | (103) |   |                                   |     |    |    |           |

5

**Figure 25B**

|               |       |  |       |    |    |    | Section 1 |
|---------------|-------|--|-------|----|----|----|-----------|
|               | (1)   | 10   | 20    | 30 | 40 | 52 |           |
| CR2-1.17.1_LC | (1)   | DIQMTQSPSSLSASVGDRVITICRASQGIRNDLGWYQQKPGKAPKRLIYAA    | 3     |    |    |    |           |
| A30           | (1)   | DIQMTQSPSSLSASVGDRVITICRASQGIRNDLGWYQQKPGKAPKRLIYAA    | 3     |    |    |    |           |
| Consensus     | (1)   | DIQMTQSPSSLSASVGDRVITICRASQGIRNDLGWYQQKPGKAPKRLIYAA    | 3     |    |    |    |           |
|               |       |  |       |    |    |    | Section 2 |
|               | (53)  | 53   | 60    | 70 | 80 | 90 | 104       |
| CR2-1.17.1_LC | (53)  | SLQSGVPSPRFSGSGSGTEFTLTISSSLQPEDFATYYCLQHNSYPLTFGGGTKV |       |    |    |    |           |
| A30           | (53)  | SLQSGVPSPRFSGSGSGTEFTLTISSSLQPEDFATYYCLQHNSYF          | ----- |    |    |    |           |
| Consensus     | (53)  | SLQSGVPSPRFSGSGSGTEFTLTISSSLQPEDFATYYCLQHNSYF          |       |    |    |    |           |
|               |       |  |       |    |    |    | Section 3 |
|               | (105) | 1087   |       |    |    |    |           |
| CR2-1.17.1_LC | (105) | EIK  |       |    |    |    |           |
| A30           | (96)  | ---  |       |    |    |    |           |
| Consensus     | (105) |  |       |    |    |    |           |

**FIGURE 26**

**Figure 26A**

|             |   |     |     |    |    | Section 1 |
|-------------|---|-----|-----|----|----|-----------|
|             | (1) 1   | 10  | 20  | 30 | 40 | 52        |
| CR2-1.18_HC | (1) QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN   |     |     |    |    |           |
| VH1-8       | (1) QVOLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN   |     |     |    |    |           |
| Consensus   | (1) QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN   |     |     |    |    |           |
|             |   |     |     |    |    | Section 2 |
|             | (53) 53   | 60  | 70  | 80 | 90 | 104       |
| CR2-1.18_HC | (53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVA |     |     |    |    |           |
| VH1-8       | (53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----  |     |     |    |    |           |
| Consensus   | (53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR       |     |     |    |    |           |
|             |   |     |     |    |    | Section 3 |
|             | (105) 105   | 110 | 126 |    |    |           |
| CR2-1.18_HC | (105) GTYYYYYYGMDVWGQGTTVTVSS                             |     |     |    |    |           |
| VH1-8       | (99) -----  |     |     |    |    |           |
| Consensus   | (105)   |     |     |    |    |           |

5

**Figure 26B**

|             |  |    |    |    |    | Section 1 |
|-------------|--|----|----|----|----|-----------|
|             | (1) 1  | 10 | 20 | 30 | 40 | 53        |
| CR2-1.18_LC | (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRЛИYAASS        |    |    |    |    |           |
| A30         | (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRЛИYAASS        |    |    |    |    |           |
| Consensus   | (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRЛИYAASS        |    |    |    |    |           |
|             |  |    |    |    |    | Section 2 |
|             | (54) 54  | 60 | 70 | 80 | 90 | 106       |
| CR2-1.18_LC | (54) LQSGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYPFTFGPGTKVDI        |    |    |    |    |           |
| A30         | (54) LQSGVPSRFSGSGSGTEFTLTISLQPEDFATY <del>Y</del> CLQHNSYP----- |    |    |    |    |           |
| Consensus   | (54) LQSGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYP                   |    |    |    |    |           |
|             |  |    |    |    |    | Section 3 |
| CR2-1.18_LC | (107) <del>107</del> K   |    |    |    |    |           |
| A30         | (96) -   |    |    |    |    |           |
| Consensus   | (107)  |    |    |    |    |           |

10

**FIGURE 27**

**Figure 27A**

|                |  |     |     |    |    |           |
|----------------|--|-----|-----|----|----|-----------|
|                |  |     |     |    |    | Section 1 |
| Cur2-1.19.1_hc | (1) 1  | 10  | 20  | 30 | 40 | 52        |
| VH1-8          | (1) QVQLVQSGAEVKKPGASVVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMN |     |     |    |    |           |
| Consensus      | (1) QVQLVQSGAEVKKPGASVVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMN |     |     |    |    |           |
|                |  |     |     |    |    | Section 2 |
| Cur2-1.19.1_hc | (53) 53  | 60  | 70  | 80 | 90 | 104       |
| VH1-8          | (53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARVMITF |     |     |    |    |           |
| Consensus      | (53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR----- |     |     |    |    |           |
|                |  |     |     |    |    | Section 3 |
| Cur2-1.19.1_hc | (105) 105  | 110 | 126 |    |    |           |
| VH1-8          | (99) -----   |     |     |    |    |           |
| Consensus      | (105)  |     |     |    |    |           |

5

**Figure 27B**

|                |  |    |    |    |    |           |
|----------------|--|----|----|----|----|-----------|
|                |  |    |    |    |    | Section 1 |
| Cur2-1.19.1_lc | (1) 1  | 10 | 20 | 30 | 40 | 52        |
| A30            | (1) DIQMTQSPSSLSASVGDRVTITCRASQGIPNDLGVYQQKPGKAPKRLIYAA  |    |    |    |    |           |
| Consensus      | (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA  |    |    |    |    |           |
|                |  |    |    |    |    | Section 2 |
| Cur2-1.19.1_lc | (53) 53  | 60 | 70 | 80 | 90 | 104       |
| A30            | (53) SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFQGTLK |    |    |    |    |           |
| Consensus      | (53) SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYP-----    |    |    |    |    |           |
|                |  |    |    |    |    | Section 3 |
| Cur2-1.19.1_lc | (105) 1087   |    |    |    |    |           |
| A30            | (96) EIR   |    |    |    |    |           |
| Consensus      | (105)  |    |    |    |    |           |

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**FIGURE 28**

**Figure 28A**

|                | Section 1   |           |     |    |    |     |
|----------------|---|-----------|-----|----|----|-----|
|                | (1) 1   | 10        | 20  | 30 | 40 | 51  |
| Cur2-1.23.1_HC | (1) EVQLVQSGAEVKKPGESLKISCEGSGY3FTSYWIGWVRQMPGKGLEWMGII   |           |     |    |    |     |
| VH5-51         | (1) EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII   |           |     |    |    |     |
| Consensus      | (1) EVQLVQSGAEVKKPGESLKISC GSGYSFTSYWIGWVRQMPGKGLEWMGII   | Section 2 |     |    |    |     |
|                | (52) 52   | 60        | 70  | 80 | 90 | 102 |
| Cur2-1.23.1_HC | (52) YPGDSDTTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHVSY |           |     |    |    |     |
| VH5-51         | (52) YPGDSDTTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---  |           |     |    |    |     |
| Consensus      | (52) YPGDSDTTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR     | Section 3 |     |    |    |     |
|                | (103) 103   | 110       | 126 |    |    |     |
| Cur2-1.23.1_HC | (103) YYVSGSYNNVFDYWGQGTLTVSS                             |           |     |    |    |     |
| VH5-51         | (99) -----  |           |     |    |    |     |
| Consensus      | (103)   |           |     |    |    |     |

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**Figure 28B**

|                | Section 1   |           |    |    |    |     |
|----------------|---|-----------|----|----|----|-----|
|                | (1) 1   | 10        | 20 | 30 | 40 | 51  |
| Cur2-1.23.1_LC | (1) DIQMTQSPSSL SASVGDRVTITCRASQGIRNDLGWYQQIEPGKAPKRЛИYAA   |           |    |    |    |     |
| A30            | (1) DIQMTQSPSSL SASVGDRVTITCRASQGIRNDLGWYQQIEPGKAPKRЛИYAA   |           |    |    |    |     |
| Consensus      | (1) DIQMTQSPSSL SASVGDRVTITCRASQGIRNDLGWYQQ PGKAPKRЛИYAA    | Section 2 |    |    |    |     |
|                | (52) 52   | 60        | 70 | 80 | 90 | 102 |
| Cur2-1.23.1_LC | (52) SSLQRGVPSPRFSGSGSGTEFTLTISISSLQPEDFATYYCLOHNSYPWTFGQGT |           |    |    |    |     |
| A30            | (52) SSLQSGVPSPRFSGSGSGTEFTLTISISSLQPEDFATYYCLOHNSYP---     |           |    |    |    |     |
| Consensus      | (52) SSLQ GVPSPRFSGSGSGTEFTLTISISSLQPEDFATYYCLOHNSYP        | Section 3 |    |    |    |     |
|                | (103) 103 107   |           |    |    |    |     |
| Cur2-1.23.1_LC | (103) KVEIK   |           |    |    |    |     |
| A30            | (96) -----  |           |    |    |    |     |
| Consensus      | (103)   |           |    |    |    |     |

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**FIGURE 29**

**Figure 29A**

|               |   |     |     |    |    | Section 1 |
|---------------|---|-----|-----|----|----|-----------|
|               | (1) 1   | 10  | 20  | 30 | 40 | 51        |
| CR2-1.24.1_HC | (1) QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADI   |     |     |    |    |           |
| VH3-33        | (1) QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVI   |     |     |    |    |           |
| Consensus     | (1) QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVA I   |     |     |    |    |           |
|               |   |     |     |    |    | Section 2 |
|               | (52) 52   | 60  | 70  | 80 | 90 | 102       |
| CR2-1.24.1_HC | (52) WYDGSNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY |     |     |    |    |           |
| VH3-33        | (52) WYDGSNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---  |     |     |    |    |           |
| Consensus     | (52) WYDGSNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR     |     |     |    |    |           |
|               |   |     |     |    |    | Section 3 |
|               | (103) 103   | 110 | 120 |    |    |           |
| CR2-1.24.1_HC | (103) SYGYVYYDYGMDVWGQGTTTVSS                             |     |     |    |    |           |
| VH3-33        | (99) -----  |     |     |    |    |           |
| Consensus     | (103)   |     |     |    |    |           |

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**Figure 29B**

|               |  |    |    |    |    | Section 1 |
|---------------|--|----|----|----|----|-----------|
|               | (1) 1  | 10 | 20 | 30 | 40 | 52        |
| CR2-1.24.1_LC | (1) DIQMTQSPSSLSASVGDRVТИCRASQGIRNDLGWYQQKPGKAPKRЛИЯАС   |    |    |    |    |           |
| A30           | (1) DIQMTQSPSSLSASVGDRVТИCRASQGIRNDLGWYQQKPGKAPKRЛИЯАС   |    |    |    |    |           |
| Consensus     | (1) DIQMTQSPSSLSASVGDRVТИCRASQGIRNDLGWYQQKPGKAPKRЛИЯАС   |    |    |    |    |           |
|               |  |    |    |    |    | Section 2 |
|               | (53) 53  | 60 | 70 | 80 | 90 | 104       |
| CR2-1.24.1_LC | (53) SLQSGVPSSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTV |    |    |    |    |           |
| A30           | (53) SLQSGVPSSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP-----    |    |    |    |    |           |
| Consensus     | (53) SLQSGVPSSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP         |    |    |    |    |           |
|               |  |    |    |    |    | Section 3 |
|               | (105) 1067   |    |    |    |    |           |
| CR2-1.24.1_LC | (105) EIK  |    |    |    |    |           |
| A30           | (96) ---   |    |    |    |    |           |
| Consensus     | (105)  |    |    |    |    |           |

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**FIGURE 30**

**Figure 30A**

|               | (1)   | 10                       | 20      | 30                       | 40 | 51                     | Section 1 |
|---------------|-------|--------------------------|---------|--------------------------|----|------------------------|-----------|
| VH5-51        | (1)   | EVQLVQSGAEVKKPGESLKI     | SCKGSGY | SFTSYWIGWVRQMPGKGLEWMGII |    |                        |           |
| CR2-1.25.1_HC | (1)   | EVQLVQSGAEVKKPGESLKI     | SCKGSGY | RFTSYWIGWVRQMPGKGLEWMGII |    |                        |           |
| Consensus     | (1)   | EVQLVQSGAEVKKPGESLKI     | SCKGSGY | FTSYWIGWVRQMPGKGLEWMGII  |    |                        |           |
|               | (52)  | 60                       | 70      | 80                       | 90 | 102                    | Section 2 |
| VH5-51        | (52)  | YFGDSDTRYSPSFQGQVTISADKS | I       | SADKS                    | I  | STAYLQWSSLKASDTAMYYCAR | ---       |
| CR2-1.25.1_HC | (52)  | YFGDSDTRYSPSFQGQVTISADKS | I       | SADKS                    | I  | STAYLQWSSLKASDTAMYYCAR | HGSY      |
| Consensus     | (52)  | YFGDSDTRYSPSFQGQVTISADKS | I       | SADKS                    | I  | STAYLQWSSLKASDTAMYYCAR |           |
|               | (103) | 103                      | 110     | 126                      |    |                        | Section 3 |
| VH5-51        | (99)  | ---                      | ---     | ---                      |    |                        |           |
| CR2-1.25.1_HC | (103) | YYGSETYYNVFDYWGQGTLVTVSS |         |                          |    |                        |           |
| Consensus     | (103) |                          |         |                          |    |                        |           |

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**Figure 30B**

|               | (1)   | 10                       | 20        | 30                | 40       | 52    | Section 1 |
|---------------|-------|--------------------------|-----------|-------------------|----------|-------|-----------|
| A30           | (1)   | DIQMTQSPSSLSASVGDRVTITCR | ASQGIRNDL | GWYQQKEGKAPKR     | R        | LIYAA | S         |
| CR2-1.25.1_LC | (1)   | DIQMTQSPSSLSASVGDRVTITCR | ASQGIRNDL | GWYQQKEGKAPKR     | R        | LIYAA | S         |
| Consensus     | (1)   | DIQMTQSPSSLSASVGDRVTITCR | ASQGIRNDL | GWYQQKEGKAPKR     | R        | LIYAA | S         |
|               | (53)  | 53                       | 60        | 70                | 80       | 90    | 104       |
| A30           | (53)  | SLQSGVPSRFSGSGSGTEFTL    | TISL      | QPEDFATYYCLQHNSYP | ---      | ---   |           |
| CR2-1.25.1_LC | (53)  | SLQSGVPSRFSGSGSGTEFTL    | TISL      | QPEDFATYYCLQHNSYP | WTFGQGTV |       |           |
| Consensus     | (53)  | SLQSGVPSRFSGSGSGTEFTL    | TISL      | QPEDFATYYCLQHNSYP |          |       |           |
|               | (105) | 1087                     |           |                   |          |       | Section 3 |
| A30           | (96)  | ---                      |           |                   |          |       |           |
| CR2-1.25.1_LC | (105) | EIK                      |           |                   |          |       |           |
| Consensus     | (105) |                          |           |                   |          |       |           |

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**FIGURE 31**

**Figure 31A**

|             |  |                      |           |     |    | Section 1 |
|-------------|--|----------------------|-----------|-----|----|-----------|
|             | (1) 1  | 10                   | 20        | 30  | 40 | 52        |
| VH5-51      | (1) EVQLVQSGAEVKKPGE <del>SLKISCKGSGY</del> SFTSYWIGWVRQMPGKGLEWMGIY |                      |           |     |    |           |
| CR2-1.29_HC | (1) EVQLVQSGAEVKKPGE <del>SLKISCKGSGY</del> SFTSYWIGWVRQMPGKGLEWMGIY |                      |           |     |    |           |
| Consensus   | (1) EVQLVQSGAEVKKPGE <del>SLKISCKGSGY</del> SFTSYWIGWVRQMPGKGLEWMGIY |                      |           |     |    |           |
|             |  |                      |           |     |    | Section 2 |
|             | (53) 53  | 60                   | 70        | 80  | 90 | 104       |
| VH5-51      | (53) PGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKA                            | SDTAMYCAR            | -----     |     |    |           |
| CR2-1.29_HC | (53) PGDSDTRYSPSFQGQATISADKSISTAYLQWSSLKA                            | SDTAMYCAR            | HVDVGA    |     |    |           |
| Consensus   | (53) PGDSDTRYSPSFQGQ   | TISADKSISTAYLQWSSLKA | SDTAMYCAR |     |    |           |
|             |  |                      |           |     |    | Section 3 |
|             | (105) 105  | 110                  |           | 129 |    |           |
| VH5-51      | (99) -----   |                      |           |     |    |           |
| CR2-1.29_HC | (105) TIGGYYYYYHGMDEVWGQGTTVTVSS                                     |                      |           |     |    |           |
| Consensus   | (105)  |                      |           |     |    |           |

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**Figure 31B**

|             |  |       |    |    |    | Section 1 |
|-------------|--|-------|----|----|----|-----------|
|             | (1) 1  | 10    | 20 | 30 | 40 | 53        |
| A19         | (1) DIVMTQSP <del>LSLPVTPGEPASISCRSSQ</del> SLHSNGYNYLDWYI <del>QKPGQSP</del> Q <del>PLL</del> |       |    |    |    |           |
| CR2-1.29_LC | (1) DIVMTQSP <del>LSLPVTPGEPASISCRSSQ</del> SLHSNGYNYLDWYI <del>QKPGQSP</del> Q <del>PLL</del> |       |    |    |    |           |
| Consensus   | (1) DIVMTQSP <del>LSLPVTPGEPASISCRSSQ</del> SLHSNGYNYLDWYI <del>QKPGQSP</del> Q <del>PLL</del> |       |    |    |    |           |
|             |  |       |    |    |    | Section 2 |
|             | (54) 54  | 60    | 70 | 80 | 90 | 106       |
| A19         | (54) YLGSNRASGV <del>PDRFSGSGSGTDFTLKISRVEAEDVGVY</del> YCMQALQ <del>TP</del>                  | ----- |    |    |    |           |
| CR2-1.29_LC | (54) YLGSNRASGV <del>PDRFSGSGSGTDFTLKISRVEAEDVGVY</del> YCMQALQ <del>SLMC</del> SFGQ           |       |    |    |    |           |
| Consensus   | (54) YLGSNRASGV <del>PDRFSGSGSGTDFTLKISRVEAEDVGVY</del> YCMQALQ <del>S</del>                   |       |    |    |    |           |
|             |  |       |    |    |    | Section 3 |
|             | (107) 107  | 113   |    |    |    |           |
| A19         | (101) -----  |       |    |    |    |           |
| CR2-1.29_LC | (107) GTKLEIK  |       |    |    |    |           |
| Consensus   | (107)  |       |    |    |    |           |

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**FIGURE 32**

**Figure 32A**

|             |   |     |     |     |    | Section 1 |
|-------------|---|-----|-----|-----|----|-----------|
|             | (1) 1   | 10  | 20  | 30  | 40 | 52        |
| VH1-18      | (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMWVRQAPGQGLEWMGWIS |     |     |     |    |           |
| CR2-1.33_HC | (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMWVRQAPGQGLEWMGWIS |     |     |     |    |           |
| Consensus   | (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMWVRQAPGQGLEWMGWIS |     |     |     |    |           |
|             |   |     |     |     |    | Section 2 |
|             | (53) 53   | 60  | 70  | 80  | 90 | 104       |
| VH1-18      | (53) AYNGNTNYAQKLQGRVTMTTDSTSTAYMELRSILRSDDTAVYYCAR-----  |     |     |     |    |           |
| CR2-1.33_HC | (53) AYNGNTNYAQKLQGRVTMTTDSTSTAYMELRSILRSDDTAVYYCARDHYDS  |     |     |     |    |           |
| Consensus   | (53) AYNGNTNYAQKLQGRVTMTTDSTSTAYMELRSILRSDDTAVYYCAR       |     |     |     |    |           |
|             |   |     |     |     |    | Section 3 |
|             | (105) 105   | 110 | 120 | 127 |    |           |
| VH1-18      | (99) -----  |     |     |     |    |           |
| CR2-1.33_HC | (105) SDYLYYYYGLDVWGQGTTTVSS                              |     |     |     |    |           |
| Consensus   | (105)   |     |     |     |    |           |

5

**Figure 32B**

|             |   |    |    |    |    | Section 1 |
|-------------|---|----|----|----|----|-----------|
|             | (1) 1   | 10 | 20 | 30 | 40 | 53        |
| A20         | (1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAST   |    |    |    |    |           |
| CR2-1.33_LC | (1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAST   |    |    |    |    |           |
| Consensus   | (1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAST   |    |    |    |    |           |
|             |   |    |    |    |    | Section 2 |
|             | (54) 54   | 60 | 70 | 80 | 90 | 106       |
| A20         | (54) LQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYN SAP-----       |    |    |    |    |           |
| CR2-1.33_LC | (54) LQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYN SAPLTFGGGTKVEI |    |    |    |    |           |
| Consensus   | (54) LQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYN SAP            |    |    |    |    |           |
|             |   |    |    |    |    | Section 3 |
| A20         | (107) R   |    |    |    |    |           |
| CR2-1.33_LC | (107) R   |    |    |    |    |           |
| Consensus   | (107)   |    |    |    |    |           |

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**FIGURE 33**

**Figure 33A**

|               | Section 1  |     |     |     |    |     |
|---------------|--|-----|-----|-----|----|-----|
|               | (1) 1  | 10  | 20  | 30  | 40 | 51  |
| VH3-33        | (1) QVQLVESGGGVVQPGRLSRLSCAASGFTFSYYGMHWVRQAPGKGLEWVAVI  |     |     |     |    |     |
| CR2-1.38.1_HC | (1) QVQLVESGGGVVQPGRLSRLSCAASGFTFSYYGMHWVRQAPGKGLEWVAII  |     |     |     |    |     |
| Consensus     | (1) QVQLVESGGGVVQPGRLSRLSCAASGFTFSYYGMHWVRQAPGKGLEWVAII  |     |     |     |    |     |
|               | Section 2  |     |     |     |    |     |
|               | (52) 52  | 60  | 70  | 80  | 90 | 102 |
| VH3-33        | (52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---  |     |     |     |    |     |
| CR2-1.38.1_HC | (52) WYDGNDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYYY |     |     |     |    |     |
| Consensus     | (52) WYDG KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR      |     |     |     |    |     |
|               | Section 3  |     |     |     |    |     |
|               | (103) 103  | 110 | 120 | 127 |    |     |
| VH3-33        | (99) -----   |     |     |     |    |     |
| CR2-1.38.1_HC | (103) DSSDYLYYYYGMDVWGQTTVTVS                            |     |     |     |    |     |
| Consensus     | (103)  |     |     |     |    |     |

5

**Figure 33B**

|               | Section 1  |     |                      |            |    |     |
|---------------|--|-----|----------------------|------------|----|-----|
|               | (1) 1  | 10  | 20                   | 30         | 40 | 52  |
| A20           | (1) DIQMTQSPSSLSASVGDRVITITCRASQGISNYLAWYQQKPGKVPKLLIYAA |     |                      |            |    |     |
| CR2-1.38.1_LC | (1) DIQMTQSPSSLSASVGDRVITITCRASQGISNYLAWYQQKPGKVPNLLIYAA |     |                      |            |    |     |
| Consensus     | (1) DIQMTQSPSSLSASVGDRVITITCRASQGISNYLAWYQQKPGKVP LLIYAA |     |                      |            |    |     |
|               | Section 2  |     |                      |            |    |     |
|               | (53) 53  | 60  | 70                   | 80         | 90 | 104 |
| A20           | (53) TLQSGVP SRFSGSGSGTDF                                | TLT | ISLQPEDVATYYCQKYN    | SAP-----   |    |     |
| CR2-1.38.1_LC | (53) TLQSGVP SRFSGSGSGTDF                                | SLT | ISLQPEDVAAYYCQKCNSA  | PWTFGQGTTV |    |     |
| Consensus     | (53) TLQSGVP SRFSGSGSGTDF                                | SLT | ISLQPEDVA YYCQK NSAP |            |    |     |
|               | Section 3  |     |                      |            |    |     |
|               | (105) 1067   |     |                      |            |    |     |
| A20           | (96) ---   |     |                      |            |    |     |
| CR2-1.38.1_LC | (105) EIK  |     |                      |            |    |     |
| Consensus     | (105)  |     |                      |            |    |     |

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**FIGURE 34**

**Figure 34A**

|               | Section 1 |                              |                    |                   |                   |       |             |     |    |    |     |
|---------------|-----------|------------------------------|--------------------|-------------------|-------------------|-------|-------------|-----|----|----|-----|
|               | 1         | 10                           | 20                 | 30                | 40                | 50    | 60          | 70  | 80 | 90 | 100 |
| VH5-51        | (1)       | EVQLVQSGAEVKKPGESLKISCKGSGYF | TSYWI              | GWVRQMPGKGLEWMGII |                   |       |             |     |    |    |     |
| CR2-1.39.1_HC | (1)       | EVQLVQSGTEVKKPGE             | SLKISCKGSGYRFT     | TSYWI             | GWVRQMPGKGLEWMGII |       |             |     |    |    |     |
| Consensus     | (1)       | EVQLVQSG                     | EVKKPGESLKISCKGSGY | FT8YWI            | GWVRQMPGKGLEWMGII |       |             |     |    |    |     |
|               | Section 2 |                              |                    |                   |                   |       |             |     |    |    |     |
|               | 52        | 60                           | 70                 | 80                | 90                | 100   | 102         |     |    |    |     |
| VH5-51        | (52)      | YFGDSDTRYSPSFQGQVT           | ISADKS             | IS                | STAYLQ            | WSSLK | ASDTAMYYCAR | --- |    |    |     |
| CR2-1.39.1_HC | (52)      | YFGDSDTRYSPSFQGQVT           | ISADKS             | IS                | STAYLQ            | WSSLK | ASDTAMYYCAR | HG  |    |    |     |
| Consensus     | (52)      | YFGDSDTRYSPSFQGQVT           | ISADKS             | IS                | STAYLQ            | WSSLK | ASDTAMYYCAR |     |    |    |     |
|               | Section 3 |                              |                    |                   |                   |       |             |     |    |    |     |
|               | 103       | 110                          | 126                |                   |                   |       |             |     |    |    |     |
| VH5-51        | (103)     | YYNSGSYYNVFDXWGGQTLVTVSS     |                    |                   |                   |       |             |     |    |    |     |
| CR2-1.39.1_HC | (103)     | YYNSGSYYNVFDXWGGQTLVTVSS     |                    |                   |                   |       |             |     |    |    |     |
| Consensus     | (103)     | YYNSGSYYNVFDXWGGQTLVTVSS     |                    |                   |                   |       |             |     |    |    |     |

5

**Figure 34B**

|               | Section 1 |   |    |                     |           |     |     |    |    |    |     |
|---------------|-----------|---|----|---------------------|-----------|-----|-----|----|----|----|-----|
|               | 1         | 10  | 20 | 30                  | 40        | 50  | 60  | 70 | 80 | 90 | 100 |
| A30           | (1)       | DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAS |    |                     |           |     |     |    |    |    |     |
| CR2-1.39.1_LC | (1)       | DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAS |    |                     |           |     |     |    |    |    |     |
| Consensus     | (1)       | DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAS |    |                     |           |     |     |    |    |    |     |
|               | Section 2 |   |    |                     |           |     |     |    |    |    |     |
|               | 53        | 60  | 70 | 80                  | 90        | 100 | 104 |    |    |    |     |
| A30           | (53)      | SLQSGVP3RFSGSGSGTEFTLT                              | IS | SLQPEDFATYYCLQHNSYP |           |     |     |    |    |    |     |
| CR2-1.39.1_LC | (53)      | SLQSGVP3RFSGSGSGTEFTLT                              | IS | SLQPEDFATYYCLQHNSYP | WTFGQGTRV |     |     |    |    |    |     |
| Consensus     | (53)      | SLQSGVP3RFSGSGSGTEFTLT                              | IS | SLQPEDFATYYCLQHNSYP |           |     |     |    |    |    |     |
|               | Section 3 |   |    |                     |           |     |     |    |    |    |     |
|               | 105       | 1097  |    |                     |           |     |     |    |    |    |     |
| A30           | (96)      | ---   |    |                     |           |     |     |    |    |    |     |
| CR2-1.39.1_LC | (105)     | EIK   |    |                     |           |     |     |    |    |    |     |
| Consensus     | (105)     | EIK   |    |                     |           |     |     |    |    |    |     |

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**FIGURE 35**

**Figure 35A**

|             |       |  |     |    |     |    |  |  |  |  | Section 1 |
|-------------|-------|--|-----|----|-----|----|--|--|--|--|-----------|
| VH1-8       | (1)   | 1  | 10  | 20 | 30  | 40 |  |  |  |  | 52        |
| CR2-1.45_HC | (1)   | QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN |     |    |     |    |  |  |  |  |           |
| Consensus   | (1)   | QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN |     |    |     |    |  |  |  |  |           |
|             |       |  |     |    |     |    |  |  |  |  | Section 2 |
| VH1-8       | (53)  | 53   | 60  | 70 | 80  | 90 |  |  |  |  | 104       |
| CR2-1.45_HC | (53)  | PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----  |     |    |     |    |  |  |  |  |           |
| Consensus   | (53)  | PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGSY  |     |    |     |    |  |  |  |  |           |
|             |       |  |     |    |     |    |  |  |  |  | Section 3 |
| VH1-8       | (105) | 105  | 110 |    | 125 |    |  |  |  |  |           |
| CR2-1.45_HC | (105) | GYDYYYYGMDVWGQGTTTVSS                                |     |    |     |    |  |  |  |  |           |
| Consensus   | (105) |  |     |    |     |    |  |  |  |  |           |

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**Figure 35B**

|             |       |   |    |    |    |    |  |  |  |  | Section 1 |
|-------------|-------|---|----|----|----|----|--|--|--|--|-----------|
| A20         | (1)   | 1   | 10 | 20 | 30 | 40 |  |  |  |  | 53        |
| CR2-1.45_LC | (1)   | DIQMTQSPSSLSAVGDRVTITCRASQGISNYLAWYQQKPGKVKPLLIYAAST    |    |    |    |    |  |  |  |  |           |
| Consensus   | (1)   | DIQMTQSPSSLSAVGDRVTI CRASQGISN LAWYQQKPGKVKPLLIYAAST    |    |    |    |    |  |  |  |  |           |
|             |       |   |    |    |    |    |  |  |  |  | Section 2 |
| A20         | (54)  | 54  | 60 | 70 | 80 | 90 |  |  |  |  | 106       |
| CR2-1.45_LC | (54)  | LQSGVPSRFSGSGSGTDFLTITISSLQPEDVATYYCQKYN SAP-----       |    |    |    |    |  |  |  |  |           |
| Consensus   | (54)  | LQLGVPSRFSGSGSGTDFLTITISSLQPEDVATYYCQKYN SAPFTPGPGTKVDI |    |    |    |    |  |  |  |  |           |
|             |       |   |    |    |    |    |  |  |  |  | Section 3 |
| A20         | (107) | 107   |    |    |    |    |  |  |  |  |           |
| CR2-1.45_LC | (107) | R   |    |    |    |    |  |  |  |  |           |
| Consensus   | (107) |   |    |    |    |    |  |  |  |  |           |

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**FIGURE 36**

**Figure 36A**

|               |  |     |     |    |    | Section 1 |
|---------------|--|-----|-----|----|----|-----------|
|               | 1  | 10  | 20  | 30 | 40 | 51        |
| VH1-8         | (1) QVQLVQSGAEVKKPGASVKSCKASGYTFTSYDINWVRQATGQGLEWMGWM     |     |     |    |    |           |
| CR2-1.46.1_HC | (1) QVQLVQSGAEVKKPGASVKSCKASGYGFTSYDINWVRQATGQGLEWMGWM     |     |     |    |    |           |
| Consensus     | (1) QVQLVQSGAEVKKPGASVKSCKASGYGFTSYDINWVRQATGQGLEWMGWM     |     |     |    |    |           |
|               |  |     |     |    |    | Section 2 |
|               | 52   | 60  | 70  | 80 | 90 | 102       |
| VH1-8         | (52) NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR---    |     |     |    |    |           |
| CR2-1.46.1_HC | (52) NPNNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR DIVV |     |     |    |    |           |
| Consensus     | (52) NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR       |     |     |    |    |           |
|               |  |     |     |    |    | Section 3 |
|               | 103  | 110 | 126 |    |    |           |
| VH1-8         | (103) (99) -----   |     |     |    |    |           |
| CR2-1.46.1_HC | (103) VVTATDYYYGMDVWGQTTVTVSS                              |     |     |    |    |           |
| Consensus     | (103)  |     |     |    |    |           |

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**Figure 36B**

|               |   |      |    |    |    | Section 1 |
|---------------|---|------|----|----|----|-----------|
|               | 1   | 10   | 20 | 30 | 40 | 52        |
| A30           | (1) DIQMTQSP3SLASAVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA |      |    |    |    |           |
| CR2-1.46.1_LC | (1) DIQMTQSP3SLASAVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA |      |    |    |    |           |
| Consensus     | (1) DIQMTQSP3SLASAVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA |      |    |    |    |           |
|               |   |      |    |    |    | Section 2 |
|               | 53  | 60   | 70 | 80 | 90 | 104       |
| A30           | (53) SLQSGVPSPRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP-----   |      |    |    |    |           |
| CR2-1.46.1_LC | (53) SLPSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHSGYPPTFGQGTV |      |    |    |    |           |
| Consensus     | (53) SL SGVPSPRFSGSGSGTEFTLTISLQPEDFATYYCLQH YP         |      |    |    |    |           |
|               |   |      |    |    |    | Section 3 |
|               | 105   | 1067 |    |    |    |           |
| A30           | (96) ---  |      |    |    |    |           |
| CR2-1.46.1_LC | (105) EIK   |      |    |    |    |           |
| Consensus     | (105)   |      |    |    |    |           |

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**FIGURE 37**

**Figure 37A**

|               | Section 1  |     |     |    |    |     |
|---------------|--|-----|-----|----|----|-----|
|               | (1) 1  | 10  | 20  | 30 | 40 | 51  |
| CR2-1.48.1_HC | (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMWVRQAPGQGLEWMGWI |     |     |    |    |     |
| VH1-18        | (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMWVRQAPGQGLEWMGWI |     |     |    |    |     |
| Consensus     | (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMWVRQAPGQGLEWMGWI |     |     |    |    |     |
|               | Section 2  |     |     |    |    |     |
|               | (2) 52   | 60  | 70  | 80 | 90 | 102 |
| CR2-1.48.1_HC | (2) SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEY  |     |     |    |    |     |
| VH1-18        | (2) SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR---   |     |     |    |    |     |
| Consensus     | (2) SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR      |     |     |    |    |     |
|               | Section 3  |     |     |    |    |     |
|               | (103) 103  | 110 | 125 |    |    |     |
| CR2-1.48.1_HC | (103) YYDGSGYYYFDYWGQGLVTVSS                             |     |     |    |    |     |
| VH1-18        | (99) -----   |     |     |    |    |     |
| Consensus     | (103)  |     |     |    |    |     |

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**Figure 37B**

|               | Section 1   |    |    |    |    |     |
|---------------|---|----|----|----|----|-----|
|               | (1) 1   | 10 | 20 | 30 | 40 | 52  |
| CR2-1.48.1_LC | (1) DIQMTQSPSSVSASVGDRVITITCRASQGIISSWLAWYQQKPGKAPKLLIYAS |    |    |    |    |     |
| L5            | (1) DIQMTQSPSSVSASVGDRVITITCRASQGIISSWLAWYQQKPGKAPKLLIYAS |    |    |    |    |     |
| Consensus     | (1) DIQMTQSPSSVSASVGDRVITITCRASQGIISSWLAWYQQKPGKAPKLLIYAS |    |    |    |    |     |
|               | Section 2   |    |    |    |    |     |
|               | (53) 53   | 60 | 70 | 80 | 90 | 104 |
| CR2-1.48.1_LC | (53) ILQSGVPBRFSGSGSGTDFTLTISLQPEDFASYYCQQANSFPRTFGQGCKV  |    |    |    |    |     |
| L5            | (53) ILQSGVPBRFSGSGSGTDFTLTISLQPEDFASYYCQQANSFP-----      |    |    |    |    |     |
| Consensus     | (53) LQSGVPBRFSGSGSGTDFTLTISLQPEDFASYYCQQANSFP            |    |    |    |    |     |
|               | Section 3   |    |    |    |    |     |
|               | (105) 1087  |    |    |    |    |     |
| CR2-1.48.1_LC | (105) EIK   |    |    |    |    |     |
| L5            | (96) ---  |    |    |    |    |     |
| Consensus     | (105)   |    |    |    |    |     |

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**FIGURE 38**

**Figure 38A**

|               | 1     | 10  | 20  | 30 | 40 | 51  | Section 1 |
|---------------|-------|---|-----|----|----|-----|-----------|
| CR2-1.49.1_HC | (1)   | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM  |     |    |    |     |           |
| VH1-8         | (1)   | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM  |     |    |    |     |           |
| Consensus     | (1)   | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM  |     |    |    |     |           |
|               | 52    | 60  | 70  | 80 | 90 | 102 | Section 2 |
| CR2-1.49.1_HC | (52)  | NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDI |     |    |    |     |           |
| VH1-8         | (52)  | NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR---  |     |    |    |     |           |
| Consensus     | (52)  | NPNSG TGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR     |     |    |    |     |           |
|               | 103   | 110   | 127 |    |    |     | Section 3 |
| CR2-1.49.1_HC | (103) | VATSYYYFYGMDVWGQGTTTVSS                             |     |    |    |     |           |
| VH1-8         | (99)  | -----   |     |    |    |     |           |
| Consensus     | (103) |   |     |    |    |     |           |

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**Figure 38B**

|               | 1     | 10   | 20 | 30 | 40 | 52  | Section 1 |
|---------------|-------|--|----|----|----|-----|-----------|
| CR2-1.49.1_LC | (1)   | DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLLKPGQSPQL   |    |    |    |     |           |
| A19           | (1)   | DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLLKPGQSPQL   |    |    |    |     |           |
| Consensus     | (1)   | DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLL KPGQSPQL  |    |    |    |     |           |
|               | 53    | 60   | 70 | 80 | 90 | 104 | Section 2 |
| CR2-1.49.1_LC | (53)  | IYLG88RASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQTLQITFGQ |    |    |    |     |           |
| A19           | (53)  | IYLG88RASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP--- |    |    |    |     |           |
| Consensus     | (53)  | IYLG8 RASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQ LQTP    |    |    |    |     |           |
|               | 105   | 111  |    |    |    |     | Section 3 |
| CR2-1.49.1_LC | (105) | GTRLEIK  |    |    |    |     |           |
| A19           | (101) | -----  |    |    |    |     |           |
| Consensus     | (105) |  |    |    |    |     |           |

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**FIGURE 39**

**Figure 39A**

|               |  |     |     |    |    | Section 1 |
|---------------|--|-----|-----|----|----|-----------|
|               | (1) 1  | 10  | 20  | 30 | 40 | 51        |
| CR2-1.51.1_HC | (1) EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII                  |     |     |    |    |           |
| VH5-51        | (1) EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII                  |     |     |    |    |           |
| Consensus     | (1) EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII                  |     |     |    |    |           |
|               |  |     |     |    |    | Section 2 |
|               | (52) 52  | 60  | 70  | 80 | 90 | 102       |
| CR2-1.51.1_HC | (52) YFGDSDA <b>KYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHYDY</b>         |     |     |    |    |           |
| VH5-51        | (52) YFGDSD <b>T</b> <b>RYSFSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR</b> --- |     |     |    |    |           |
| Consensus     | (52) YFGDSD <b>KYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR</b>              |     |     |    |    |           |
|               |  |     |     |    |    | Section 3 |
|               | (103) 103  | 110 | 120 |    |    |           |
| CR2-1.51.1_HC | (103) VWRNYRYTGWFDPWGQGT <del>L</del> TVSS                               |     |     |    |    |           |
| VH5-51        | (99) -----   |     |     |    |    |           |
| Consensus     | (103)  |     |     |    |    |           |

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**Figure 39B**

|               |  |    |    |    |    | Section 1 |
|---------------|--|----|----|----|----|-----------|
|               | (1) 1  | 10 | 20 | 30 | 40 | 52        |
| CR2-1.51.1_LC | (1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA |    |    |    |    |           |
| A27           | (1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA |    |    |    |    |           |
| Consensus     | (1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA |    |    |    |    |           |
|               |  |    |    |    |    | Section 2 |
|               | (53) 53  | 60 | 70 | 80 | 90 | 104       |
| CR2-1.51.1_LC | (53) SNRATGIPDRFSGSGSGTDFLTISRLPEDFAVYYCQQYGSSLFTFGPCTK  |    |    |    |    |           |
| A27           | (53) SS RATGIPDRFSGSGSGTDFLTISRLPEDFAVYYCQQYGSSP-----    |    |    |    |    |           |
| Consensus     | (53) S RATGIPDRFSGSGSGTDFLTISRLPEDFAVYYCQQYGSS           |    |    |    |    |           |
|               |  |    |    |    |    | Section 3 |
|               | (105) 10808  |    |    |    |    |           |
| CR2-1.51.1_LC | (105) VDIK   |    |    |    |    |           |
| A27           | (97) ---   |    |    |    |    |           |
| Consensus     | (105)  |    |    |    |    |           |

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**FIGURE 40**

**Figure 40A**

|               |       |   |     |    |    | Section 1 |
|---------------|-------|---|-----|----|----|-----------|
|               | 1     | 10  | 20  | 30 | 40 | 52        |
| Cur2-6.4.1 hc | (1)   | QVQLVQSGAEVKKPGASVKVSKCASGYTFTSYDINWVRQATGQGLEWMGWIN            |     |    |    |           |
| VH1-8         | (1)   | QVQLVQSGAEVKKPGASVKVSKCASGYTFTSYDINWVRQATGQGLEWMGWIN            |     |    |    |           |
| Consensus     | (1)   | QVQLVQSGAEVKKPGASVKVSKCASGYTFTSYDINWVRQATGQGLEWMGWIN            |     |    |    |           |
|               |       |   |     |    |    | Section 2 |
|               | 53    | 60  | 70  | 80 | 90 | 104       |
| Cur2-6.4.1 hc | (53)  | PNSGNTDYAQKFQGRVTMTRTSISTAYMELSSLRSEDTAIYYCVRGFGYBY             |     |    |    |           |
| VH1-8         | (53)  | PNSGNTGYAQKFQGRVTMTRTSISTAYMELSSLRSEDTA <del>VYYCAR</del> ----- |     |    |    |           |
| Consensus     | (53)  | PNSGNT YAQKFQGRVTMTR TSISTAYMELSSLRSEDTAIYYC R                  |     |    |    |           |
|               |       |   |     |    |    | Section 3 |
|               | 105   | 110   | 125 |    |    |           |
| Cur2-6.4.1 hc | (105) | NYDYYYGMDVWGQGTTTVSS  |     |    |    |           |
| VH1-8         | (99)  | -----   |     |    |    |           |
| Consensus     | (105) |   |     |    |    |           |

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**Figure 40B**

|               |       |   |    |    |    | Section 1 |
|---------------|-------|---|----|----|----|-----------|
|               | 1     | 10  | 20 | 30 | 40 | 52        |
| Cur2-6.4.1 Lc | (1)   | EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIAT |    |    |    |           |
| A27           | (1)   | EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYA |    |    |    |           |
| Consensus     | (1)   | EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYA |    |    |    |           |
|               |       |   |    |    |    | Section 2 |
|               | 53    | 60  | 70 | 80 | 90 | 104       |
| Cur2-6.4.1 Lc | (53)  | SSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGSSPCSFGQGTK |    |    |    |           |
| A27           | (63)  | SSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGS SP-----   |    |    |    |           |
| Consensus     | (53)  | SSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGS SP        |    |    |    |           |
|               |       |   |    |    |    | Section 3 |
|               | 105   | 10808   |    |    |    |           |
| Cur2-6.4.1 Lc | (105) | LEIK  |    |    |    |           |
| A27           | (97)  | -----   |    |    |    |           |
| Consensus     | (105) |   |    |    |    |           |

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**FIGURE 41**

| CLONE # | VH | #DE L | VH END | # N's | N Sequence | DH | Size of D | D Sequence | # N's | N Sequence | JH # del | JH Segment |
|---------|----|-------|--------|-------|------------|----|-----------|------------|-------|------------|----------|------------|
|---------|----|-------|--------|-------|------------|----|-----------|------------|-------|------------|----------|------------|

|       |           |    |                          |   |     |       |    |  |   |    |          |     |                            |
|-------|-----------|----|--------------------------|---|-----|-------|----|--|---|----|----------|-----|----------------------------|
| 1.19. | DP-15/1-8 | -1 | CGAGAG<br>(SEQ ID NO:92) | 3 | ACG | D3-16 | 28 | TTATGATTACGTTT<br>GGGGGAGTTATCGT<br>(SEQ ID NO:93) | 2 | GC | JH6<br>B | -12 | ACTACG<br>(SEQ ID NO:94)   |
| 1.19. | DP-15/1-8 | -1 | CGAGAG<br>(SEQ ID NO:92) | 3 | ACG | D3-16 | 28 | TTATGATTACGTTT<br>GGGGGAGTTATCGT<br>(SEQ ID NO:93) | 2 | GC | JH6<br>B | -12 | ACTACG<br>(SEQ ID NO:94)   |
| 1.19. | DP-15/1-8 | -1 | CGAGAG<br>(SEQ ID NO:92) | 3 | ACG | D3-16 | 28 | TTATGATTACGTTT<br>GGGGGAGTTATCGT<br>(SEQ ID NO:93) | 2 | GC | JH6<br>B | -12 | ACTACG<br>(SEQ ID NO:94)   |
| 6.4.1 | DP-15/1-8 | 0  | GAGAGG<br>(SEQ ID NO:95) | 3 | CTT | D5-18 | 12 | TGGATACAGCTA<br>(SEQ ID NO:96)                     | 2 | TA | JH6<br>B | 0   | ATTACTAC<br>(SEQ ID NO:97) |
| 6.4.2 | DP-15/1-8 | 0  | GAGAGG<br>(SEQ ID NO:95) | 3 | CTT | D5-18 | 12 | TGGATACAGCTA<br>(SEQ ID NO:96)                     | 2 | TA | JH6<br>B | 0   | ATTACTAC<br>(SEQ ID NO:97) |
| 6.4.3 | DP-15/1-8 | 0  | GAGAGG<br>(SEQ ID NO:95) | 3 | CTT | D5-18 | 12 | TGGATACAGCTA<br>(SEQ ID NO:96)                     | 2 | TA | JH6<br>B | 0   | ATTACTAC<br>(SEQ ID NO:97) |

| CLONE | vk | #de<br>1 | vk<br>end | #n | N SEQ | Jk | # del | JK end |
|-------|----|----------|-----------|----|-------|----|-------|--------|
|-------|----|----------|-----------|----|-------|----|-------|--------|

|            |          |    |                             |   |                             |     |    |                              |
|------------|----------|----|-----------------------------|---|-----------------------------|-----|----|------------------------------|
| 1.19.<br>1 | A30      | -3 | TTACCC<br>(SEQ ID<br>NO:98) | 6 | GTGCAG<br>(SEQ ID<br>NO:99) | JK2 | -7 | TTTTGG<br>(SEQ ID<br>NO:100) |
| 1.19.<br>2 | A30      | -3 | TTACCC<br>(SEQ ID<br>NO:98) | 6 | GTGCAG<br>(SEQ ID<br>NO:99) | JK2 | -7 | TTTTGG<br>(SEQ ID<br>NO:100) |
| 1.19.<br>3 | A30      | -3 | TTACCC<br>(SEQ ID<br>NO:98) | 6 | GTGCAG<br>(SEQ ID<br>NO:99) | JK2 | -7 | TTTTGG<br>(SEQ ID<br>NO:100) |
| 6.4.1      | A27/A27A | -3 | CTCAC<br>(SEQ ID<br>NO:98)  | 6 | GTGCAG<br>(SEQ ID<br>NO:99) | JK2 | -7 | TTTTGG<br>(SEQ ID<br>NO:100) |

| 6.4.2 | A27/A27A | -3 | NO:101)                       |   | NO:102)                      |     |    | NO:103)                      |
|-------|----------|----|-------------------------------|---|------------------------------|-----|----|------------------------------|
|       |          |    | CTCACCA<br>(SEQ ID<br>NO:101) | 6 | GTGCAG<br>(SEQ ID<br>NO:102) | JK2 | -7 | TTTTGG<br>(SEQ ID<br>NO:103) |

**FIGURE 42**

| CLONE # | VH         | #DEL | VH END                       | # N's | N Sequence     | DH    | Size of D | D Sequence                                       | # N's | N Sequence                               | JH   | # del | JH Segment                         |
|---------|------------|------|------------------------------|-------|----------------|-------|-----------|--|-------|--|------|-------|------------------------------------|
| 1.6.1   | DP-77/3-21 | 0    | GAGAGA<br>(SEQ ID<br>NO:104) | 0     | 0              | D3-16 | 22        | TATTATGATTAC<br>GTTTGGGGGA<br>(SEQ ID<br>NO:105) | 14    | ATTATCGCC<br>TCGTT<br>(SEQ ID<br>NO:106) | JH4B | -1    | CTACTT<br>(SEQ ID<br>NO:107)       |
| 1.6.1   | DP-77/3-21 | 0    | GAGAGA<br>(SEQ ID<br>NO:104) | 0     | 0              | D3-16 | 22        | TATTATGATTAC<br>GTTTGGGGGA<br>(SEQ ID<br>NO:105) | 14    | ATTATCGCC<br>TCGTT<br>(SEQ ID<br>NO:106) | JH4B | -1    | CTACTT<br>(SEQ ID<br>NO:107)       |
| 1.6.1   | DP-77/3-21 | 0    | GAGAGA<br>(SEQ ID<br>NO:104) | 0     | 0              | D3-16 | 22        | TATTATGATTAC<br>GTTTGGGGGA<br>(SEQ ID<br>NO:105) | 14    | ATTATCGCC<br>TCGTT<br>(SEQ ID<br>NO:106) | JH4B | -1    | CTACTT<br>(SEQ ID<br>NO:107)       |
| 1.11.1  | DP-42/3-53 | -5   | AGAGA<br>(SEQ ID<br>NO:108)  | 3     | GGA            | D4-17 | 10        | ACGGTGA<br>CTTTGGGGGA<br>(SEQ ID<br>NO:109)      | 5     | CGAAT<br>CGAAT<br>(SEQ ID<br>NO:110)     | JH6B | -2    | TACTACT<br>A<br>(SEQ ID<br>NO:111) |
| 1.11.2  | DP-42/3-53 | -5   | AGAGA<br>(SEQ ID<br>NO:108)  | 3     | GGA            | D4-17 | 10        | ACGGTGA<br>CTTTGGGGGA<br>(SEQ ID<br>NO:109)      | 5     | CGAAT<br>CGAAT<br>(SEQ ID<br>NO:110)     | JH6B | -2    | TACTACT<br>A<br>(SEQ ID<br>NO:111) |
| 1.23.1  | DP-73/5-51 | 0    | GAGACA<br>(SEQ ID<br>NO:112) | 18    | TGTATCGTATTACT | D3-10 | 19        | TTCGGGGAGTTA<br>TTATAAAC<br>(SEQ ID<br>NO:113)   | 2     | GT                                       | JH4B | -4    | CTTTGGA<br>(SEQ ID<br>NO:115)      |
| 1.23.2  | DP-73/5-51 | 0    | GAGACA<br>(SEQ ID<br>NO:112) | 18    | TGTATCGTATTACT | D3-10 | 19        | TTCGGGGAGTTA<br>TTATAAAC<br>(SEQ ID<br>NO:113)   | 2     | GT                                       | JH4B | -4    | CTTTGGA<br>(SEQ ID<br>NO:115)      |

| CLONE | Vk  | #del | vk end                       | #n | N SEQ | JK  | # del | JK end                        |
|-------|-----|------|------------------------------|----|-------|-----|-------|-------------------------------|
| 1.6.1 | A30 | -3   | TTACCC<br>(SEQ ID<br>NO:113) | 0  | 0     | JK4 | 0     | GCTCACT<br>(SEQ ID<br>NO:114) |

|        |            |    |   |   |   |     |    |  |
|--------|------------|----|---|---|---|-----|----|--|
| 1.6.2  | A30        | -3 | NO:116)<br>TTACCC<br>(SEQ ID<br>NO:116) | 0 | 0 | JK4 | 0  | NO:117)<br>GCTCACT<br>(SEQ ID<br>NO:117) |
| 1.6.3  | A30        | -3 | NO:116)<br>TTACCC<br>(SEQ ID<br>NO:116) | 0 | 0 | JK4 | 0  | NO:117)<br>GCTCACT<br>(SEQ ID<br>NO:117) |
| 1.11.1 | A3/A19/DPK | -4 | AAACTC<br>(SEQ ID<br>NO:118)            | 0 | 0 | JK4 | -2 | TCACTTTC<br>(SEQ ID<br>NO:119)           |
| 1.11.2 | A3/A19/DPK | -4 | AAACTC<br>(SEQ ID<br>NO:118)            | 0 | 0 | JK4 | -2 | TCACTTTC<br>(SEQ ID<br>NO:119)           |
| 1.23.1 | A30        | -3 | NO:116)<br>TTACCC<br>(SEQ ID<br>NO:120) | 0 | 0 | JK1 | 0  | GTGGAC<br>(SEQ ID<br>NO:120)             |
| 1.23.2 | A30        | -3 | NO:116)<br>TTACCC<br>(SEQ ID<br>NO:120) | 0 | 0 | JK1 | 0  | GTGGAC<br>(SEQ ID<br>NO:120)             |

DP-50/3-33 DP-50/3-33 DP-50/3-33 DP-50/3-33 DP-50/3-33 DP-50/3-33

FIGURE 43

| Clone # | VH         | # DEL | VH END                       | # N's | N Sequence                   | DH    | Size of D | D Sequence  | # N's | N Sequence                     | JH   | # del | JH Segment                     |
|---------|------------|-------|------------------------------|-------|------------------------------|-------|-----------|---|-------|--------------------------------|------|-------|--------------------------------|
| 1.17.1  | DP-50/3-33 | 0     | GAGAGA<br>(SEQ ID<br>NO:121) | 4     | TCAA                         | D5-18 | 8         | GGATACA<br>(SEQ ID<br>NO:122)                       | 9     | ATATGCTG<br>(SEQ ID<br>NO:123) | JH6B | -1    | TTACTACT<br>(SEQ ID<br>NO:124) |
| 1.17.2  | DP-50/3-33 | 0     | GAGAGA<br>(SEQ ID<br>NO:121) | 4     | TCAA                         | D5-18 | 8         | GGATACA<br>(SEQ ID<br>NO:122)                       | 9     | ATATGCTG<br>(SEQ ID<br>NO:123) | JH6B | -1    | TTACTACT<br>(SEQ ID<br>NO:124) |
| 1.17.3  | DP-50/3-33 | 0     | GAGAGA<br>(SEQ ID<br>NO:121) | 4     | TCAA                         | D5-18 | 8         | GGATACA<br>(SEQ ID<br>NO:122)                       | 9     | ATATGCTG<br>(SEQ ID<br>NO:123) | JH6B | -1    | TTACTACT<br>(SEQ ID<br>NO:124) |
| 1.18    | DP-15/1-8  | 1     | CGAGAG<br>(SEQ ID<br>NO:125) | 1     | A                            | D6-19 | 19        | GGGTATAG<br>CAGTGGCT<br>GG<br>(SEQ ID<br>NO:126)    | 4     | GACA                           | JH6B | -2    | TACTAC<br>(SEQ ID<br>NO:127)   |
| 1.24.1  | DP-50/3-33 | 0     | GAGAGA<br>(SEQ ID<br>NO:128) | 4     | TCAG                         | DK4   | 18        | GGATACAG<br>CTATGGTT<br>AC<br>(SEQ ID<br>NO:126)    | 2     | GT                             | JH6B | -4    | CTACTA<br>(SEQ ID<br>NO:130)   |
| 1.24.2  | DP-50/3-33 | 0     | GAGAGA<br>(SEQ ID<br>NO:128) | 4     | TCAG                         | DK4   | 18        | GGATACAG<br>CTATGGTT<br>AC<br>(SEQ ID<br>NO:129)    | 2     | GT                             | JH6B | -4    | CTACTA<br>(SEQ ID<br>NO:130)   |
| 1.25.1  | DP-73/5-51 | 0     | GAGACA<br>(SEQ ID<br>NO:131) | 6     | TGGATC<br>(SEQ ID<br>NO:132) | D3-10 | 30        | GTATATT<br>TGGTTCGG<br>AGACTTATT<br>ATAA<br>(SEQ ID | 3     | TGT                            | JH4B | -4    | CTTTGA<br>(SEQ ID<br>NO:135)   |

clone: 5'-GAGACA-3'  
VH: 5'-GAGACA-3'  
DH: 5'-TGATCTGG-3'  
JH: 5'-ATGATCTT-3'

| Clone # | VH         | #DEL | VH END                       | # N's | N Sequence                   | DH    | Size of DH Sequence      | # N's  | N Sequence | JH                            | # del | JH Segment |                                |
|---------|------------|------|------------------------------|-------|------------------------------|-------|--------------------------|--|------------|-------------------------------|-------|------------|--------------------------------|
| 1.25.2  | DP-73/5-51 | 0    | GAGACA<br>(SEQ ID<br>NO:131) | 6     | TGGATC<br>(SEQ ID<br>NO:132) | D3-10 | 30<br>(SEQ ID<br>NO:133) | GTATATTAA<br>TGTTTCGG<br>AGACCTATT<br>ATAA<br>(SEQ ID<br>NO:133) | 3          | TGT<br>(SEQ ID<br>NO:137)     | JH4B  | -4         | CTTTGA<br>(SEQ ID<br>NO:134)   |
| 1.29    | DP-73/5-51 | 0    | GAGACA<br>(SEQ ID<br>NO:135) | 1     | C                            | D5-12 | 21<br>(SEQ ID<br>NO:136) | GTGGATGT<br>AGGGGCT<br>ACGATT<br>(SEQ ID<br>NO:136)              | 7          | GGGGAT<br>(SEQ ID<br>NO:137)  | JH6B  | 0          | ATTACTAC<br>(SEQ ID<br>NO:138) |
| 1.33    | DP-14/1-18 | 0    | GAGAGA<br>(SEQ ID<br>NO:139) | 2     | TC                           | D21-9 | 18<br>(SEQ ID<br>NO:140) | ATTACTAT<br>GATAGTAG<br>TG<br>(SEQ ID<br>NO:140)                 | 7          | ATTATCT<br>(SEQ ID<br>NO:141) | JH6B  | -4         | CTACTA<br>(SEQ ID<br>NO:142)   |
| 1.38.1  | DP-50/3-33 | 1    | CGAGAG<br>(SEQ ID<br>NO:143) | 2     | GA                           | D21-9 | 19<br>(SEQ ID<br>NO:144) | TATTACTA<br>TGATAGTA<br>GTG<br>(SEQ ID<br>NO:144)                | 7          | ATTATCT<br>(SEQ ID<br>NO:145) | JH6B  | -4         | CTACTA<br>(SEQ ID<br>NO:146)   |
| 1.39.1  | DP-73/5-51 | 0    | GAGACA<br>(SEQ ID<br>NO:147) | 6     | TGGATC<br>(SEQ ID<br>NO:148) | D3-10 | 31<br>(SEQ ID<br>NO:149) | GTATTACT<br>ATaaTCG<br>GGGAGTTA<br>TTATAAC<br>(SEQ ID<br>NO:149) | 2          | GT<br>(SEQ ID<br>NO:149)      | JH4B  | -4         | CTTTGA<br>(SEQ ID<br>NO:150)   |
| 1.39.2  | DP-73/5-51 | 0    | GAGACA<br>(SEQ ID<br>NO:147) | 6     | TGGATC<br>(SEQ ID<br>NO:148) | D3-10 | 31<br>(SEQ ID<br>NO:149) | GTATTACT<br>ATaaTCG<br>GGGAGTTA<br>TTATAAC<br>(SEQ ID<br>NO:149) | 2          | GT<br>(SEQ ID<br>NO:149)      | JH4B  | -4         | CTTTGA<br>(SEQ ID<br>NO:150)   |
| 1.40.1  | DP-15/1-8  | 1    | CGAGAG<br>(SEQ ID<br>NO:148) | 0     | 0                            | D2    | 25<br>(SEQ ID<br>NO:149) | ATATTGTA<br>GTGGTGGT<br>(SEQ ID<br>NO:149)                       | 2          | CA<br>(SEQ ID<br>NO:149)      | JH6B  | -6         | ACTACT<br>(SEQ ID<br>NO:149)   |

| Clone # | VH         | #DEL | VH END                       | #N's | N Sequence                    | DH    | Size of D | D Sequence  | #N's | N Sequence | JH   | # del | JH Segment                   |
|---------|------------|------|------------------------------|------|-------------------------------|-------|-----------|---|------|------------|------|-------|------------------------------|
|         |            |      | NO:151)                      |      |                               |       |           |   |      |            |      |       | NO:153)                      |
| 1.40.2  | DP-15/1-8  | 1    | CGAGAG<br>(SEQ ID<br>NO:151) | 0    | 0                             | D2    | 25        | ATATTGTA<br>GTTGGTGGT<br>AGCTGCTA<br>C<br>(SEQ ID<br>NO:152)  | 2    | CA         | JH6B | -6    | ACTACT<br>(SEQ ID<br>NO:153) |
| 1.45    | DP-15/1-8  | 0    | GAGAGG<br>(SEQ ID<br>NO:154) | 2    | CA                            | DK4   | 20        | GTTGGATAC<br>AGCTATGG<br>TTAC<br>(SEQ ID<br>NO:155)           | 1    | G          | JH6B | -6    | ACTACT<br>(SEQ ID<br>NO:156) |
| 1.46.1  | DP-15/1-8  | 1    | CGAGAG<br>(SEQ ID<br>NO:157) | 0    | 0                             | D2    | 25        | ATATTGTA<br>GT<br>GGTGGTAA<br>GCTGGCTAC<br>(SEQ ID<br>NO:158) | 2    | GG         | JH6B | -6    | ACTACT<br>(SEQ ID<br>NO:159) |
| 1.46.2  | DP-15/1-8  | 1    | CGAGAG<br>(SEQ ID<br>NO:157) | 0    | 0                             | D2    | 25        | ATATTGTA<br>GTTGGTGGT<br>AGCTGCTA<br>C<br>(SEQ ID<br>NO:158)  | 2    | GG         | JH6B | -6    | ACTACT<br>(SEQ ID<br>NO:159) |
| 1.48.1  | DP-14/1-18 | 1    | CGAGAG<br>(SEQ ID<br>NO:160) | 7    | TGTTGAA<br>(SEQ ID<br>NO:161) | D21-9 | 20        | TATTACTA<br>TGAT9GTA<br>GTTGGTTAT<br>(SEQ ID<br>NO:162)       | 1    | T          | JH4B | 0     | ACTACT<br>(SEQ ID<br>NO:163) |
| 1.48.2  | DP-14/1-18 | 1    | CGAGAG<br>(SEQ ID<br>NO:160) | 7    | TGTTGAA<br>(SEQ ID<br>NO:161) | D21-9 | 20        | TATTACTA<br>TGAT9GTA<br>GTTGGTTAT<br>(SEQ ID<br>NO:162)       | 1    | T          | JH4B | 0     | ACTACT<br>(SEQ ID<br>NO:163) |

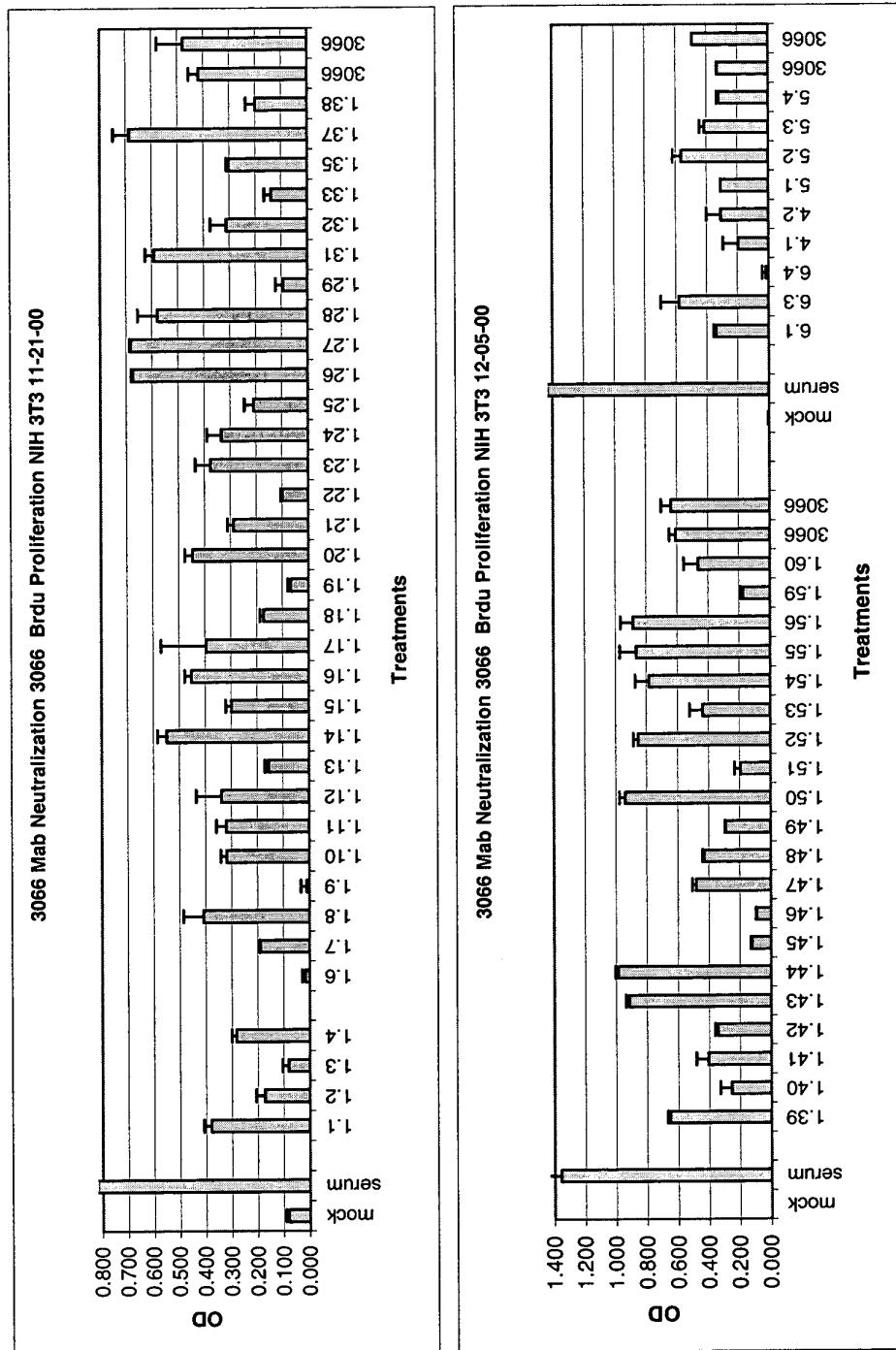
| CLONE # | VH         | #DEL | VH END                 | # N's | N Sequence            | DH    | Size of D | D Sequence  | # N's | N Sequence            | JH   | # del | JH Segment               |
|---------|------------|------|------------------------|-------|-----------------------|-------|-----------|---|-------|-----------------------|------|-------|--------------------------|
| 1.49.1  | DP-15/1-8  | 2    | GCGAGA (SEQ ID NO:164) | 5     | ATGAG (SEQ ID NO:165) | D5-12 | 17        | GGATATAG (SEQ ID NO:162)<br>TGGCTACG A                | 3     | GCT                   | JH6B | 0     | ATTACTAC (SEQ ID NO:167) |
| 1.49.2  | DP-15/1-8  | 2    | GCGAGA (SEQ ID NO:164) | 5     | ATGAG (SEQ ID NO:165) | D5-12 | 17        | GGATATAG (SEQ ID NO:166)<br>TGGCTACG A                | 3     | GCT                   | JH6B | 0     | ATTACTAC (SEQ ID NO:167) |
| 1.51.1  | DP-73/5-51 | 0    | GAGACA (SEQ ID NO:168) | 1     | C                     | D3-16 | 31        | TATGATTA (SEQ ID NO:166)<br>CGTTTGGa GGAattAT CGGTATA | 5     | CAGGG (SEQ ID NO:170) | JH5B | -5    | TGGTTC (SEQ ID NO:171)   |
| 1.51.2  | DP-73/5-51 | 0    | GAGACA (SEQ ID NO:168) | 1     | C                     | D3-16 | 31        | TATGATTA (SEQ ID NO:169)<br>CGTTTGGa GGAattAT CGGTATA | 5     | CAGGG (SEQ ID NO:170) | JH5B | -5    | TGGTTC (SEQ ID NO:171)   |

| CLONE  | VK  | #del | vk end                 | #n | N SEQ | JK  | # del | JK end                  |
|--------|-----|------|------------------------|----|-------|-----|-------|-------------------------|
| 1.17.1 | A30 | 3    | TTACCC (SEQ ID NO:172) | 0  | 0     | JK4 | 0     | GCTCACT (SEQ ID NO:173) |
| 1.17.2 | A30 | 3    | TTACCC (SEQ ID NO:172) | 0  | 0     | JK4 | 0     | GCTCACT (SEQ ID NO:173) |
| 1.17.3 | A30 | 3    | TTACCC (SEQ ID NO:172) | 0  | 0     | JK4 | 0     | GCTCACT (SEQ ID NO:173) |

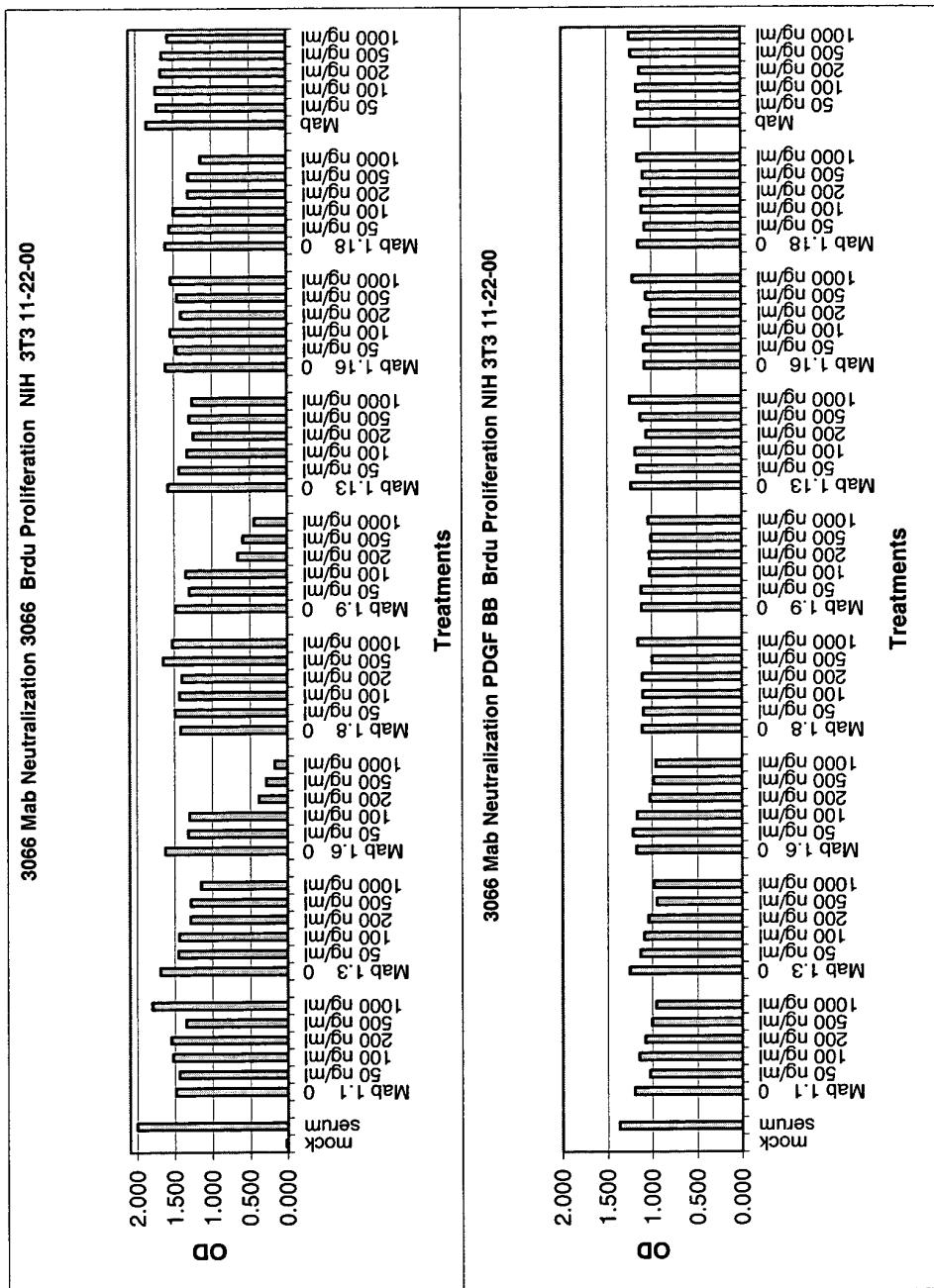
| CLONE  | vk         | #del | vk end             | #del | N SEQ                       | jk  | # del | JK end                        |
|--------|------------|------|--------------------|------|-----------------------------|-----|-------|-------------------------------|
| 1.18   | A30        | 3    | TTACCC             | 0    | 0                           | JK3 | 0     | NO:173)                       |
|        |            |      | (SEQ ID<br>NO:174) |      |                             |     |       | ATTCA C<br>(SEQ ID<br>NO:175) |
| 1.24.1 | A30        | 3    | TTACCC             | 0    | 0                           | JK1 | 0     | GTGGAC<br>(SEQ ID<br>NO:177)  |
|        |            |      | (SEQ ID<br>NO:176) |      |                             |     |       | GTGGAC<br>(SEQ ID<br>NO:177)  |
| 1.24.2 | A30        | 3    | TTACCC             | 0    | 0                           | JK1 | 0     | GTGGAC<br>(SEQ ID<br>NO:177)  |
|        |            |      | (SEQ ID<br>NO:176) |      |                             |     |       | GTGGAC<br>(SEQ ID<br>NO:177)  |
| 1.25.1 | A30        | 3    | TTACCC             | 0    | 0                           | JK1 | 0     | GTGGAC<br>(SEQ ID<br>NO:179)  |
|        |            |      | (SEQ ID<br>NO:178) |      |                             |     |       | GTGGAC<br>(SEQ ID<br>NO:179)  |
| 1.25.2 | A30        | 3    | TTACCC             | 0    | 0                           | JK1 | 0     | GTGGAC<br>(SEQ ID<br>NO:179)  |
|        |            |      | (SEQ ID<br>NO:178) |      |                             |     |       | GTGGAC<br>(SEQ ID<br>NO:179)  |
| 1.29   | A3/A19/DPK | 7    | CTACAA             | 14   | TCTCTCATG                   | JK2 | -7    | TTTGG<br>(SEQ ID<br>NO:182)   |
|        |            |      | (SEQ ID<br>NO:180) |      | TGCAG<br>(SEQ ID<br>NO:181) |     |       | TTTGG<br>(SEQ ID<br>NO:182)   |
| 1.33   | A20/DPK4   | 3    | TGCC               | 0    | 0                           | JK4 | 0     | GCTCAC<br>(SEQ ID<br>NO:184)  |
|        |            |      | (SEQ ID<br>NO:183) |      |                             |     |       | GTGGAC<br>(SEQ ID<br>NO:186)  |
| 1.38.1 | A20/DPK4   | 3    | TGCC               | 0    | 0                           | JK1 | 0     | GTGGAC<br>(SEQ ID<br>NO:188)  |
|        |            |      | (SEQ ID<br>NO:185) |      |                             |     |       | GTGGAC<br>(SEQ ID<br>NO:188)  |
| 1.39.1 | A30        | 3    | TTACCC             | 0    | 0                           | JK1 | 0     | GTGGAC<br>(SEQ ID<br>NO:188)  |
|        |            |      | (SEQ ID<br>NO:187) |      |                             |     |       | ATTCA C<br>(SEQ ID<br>NO:190) |
| 1.39.2 | A30        | 3    | TTACCC             | 0    | 0                           | JK1 | 0     | GTGGAC<br>(SEQ ID<br>NO:188)  |
|        |            |      | (SEQ ID<br>NO:187) |      |                             |     |       | GTGGAC<br>(SEQ ID<br>NO:188)  |
| 1.45   | A20/DPK4   | 3    | TGCC               | 0    | 0                           | JK3 | 0     | ATTCA C<br>(SEQ ID<br>NO:190) |
|        |            |      | (SEQ ID<br>NO:189) |      |                             |     |       | GACGTT<br>(SEQ ID             |
| 1.46.1 | A30        | 0    | CCCTCC             | 0    | 0                           | JK1 | -3    |                               |
|        |            |      | (SEQ ID            |      |                             |     |       |                               |

| CLONE  | vk         | #del | vk end                       | #n | N SEQ | jk  | # del | jk end                        |
|--------|------------|------|------------------------------|----|-------|-----|-------|-------------------------------|
|        |            |      | NO:191)                      |    |       |     |       | NO:192)                       |
| 1.46.2 | A30        | 0    | CCCTCC<br>(SEQ ID<br>NO:191) | 0  | 0     | JK1 | -3    | GACGTT<br>(SEQ ID<br>NO:192)  |
| 1.48.1 | L5/DPK5/V  | 1    | TCCCTC<br>(SEQ ID<br>NO:193) | 0  | 0     | JK1 | -2    | GGACGTT<br>(SEQ ID<br>NO:194) |
| 1.48.2 | L5/DPK5/V  | 1    | TCCCTC<br>(SEQ ID<br>NO:193) | 0  | 0     | JK1 | -2    | GGACGTT<br>(SEQ ID<br>NO:194) |
| 1.49.1 | A3/A19/DPK | 5    | CAAACT<br>(SEQ ID<br>NO:195) | 0  | 0     | JK5 | -1    | ATCACC<br>(SEQ ID<br>NO:196)  |
| 1.49.2 | A3/A19/DPK | 5    | CAAACT<br>(SEQ ID<br>NO:195) | 0  | 0     | JK5 | -1    | ATCACC<br>(SEQ ID<br>NO:196)  |
| 1.51.1 | A27/A27A   | 4    | GCTCAC<br>(SEQ ID<br>NO:197) | 1  | T     | JK3 | 0     | ATTCAC<br>(SEQ ID<br>NO:198)  |
| 1.51.1 | A27/A27A   | 4    | GCTCAC<br>(SEQ ID<br>NO:197) | 1  | T     | JK3 | 0     | ATTCAC<br>(SEQ ID<br>NO:198)  |

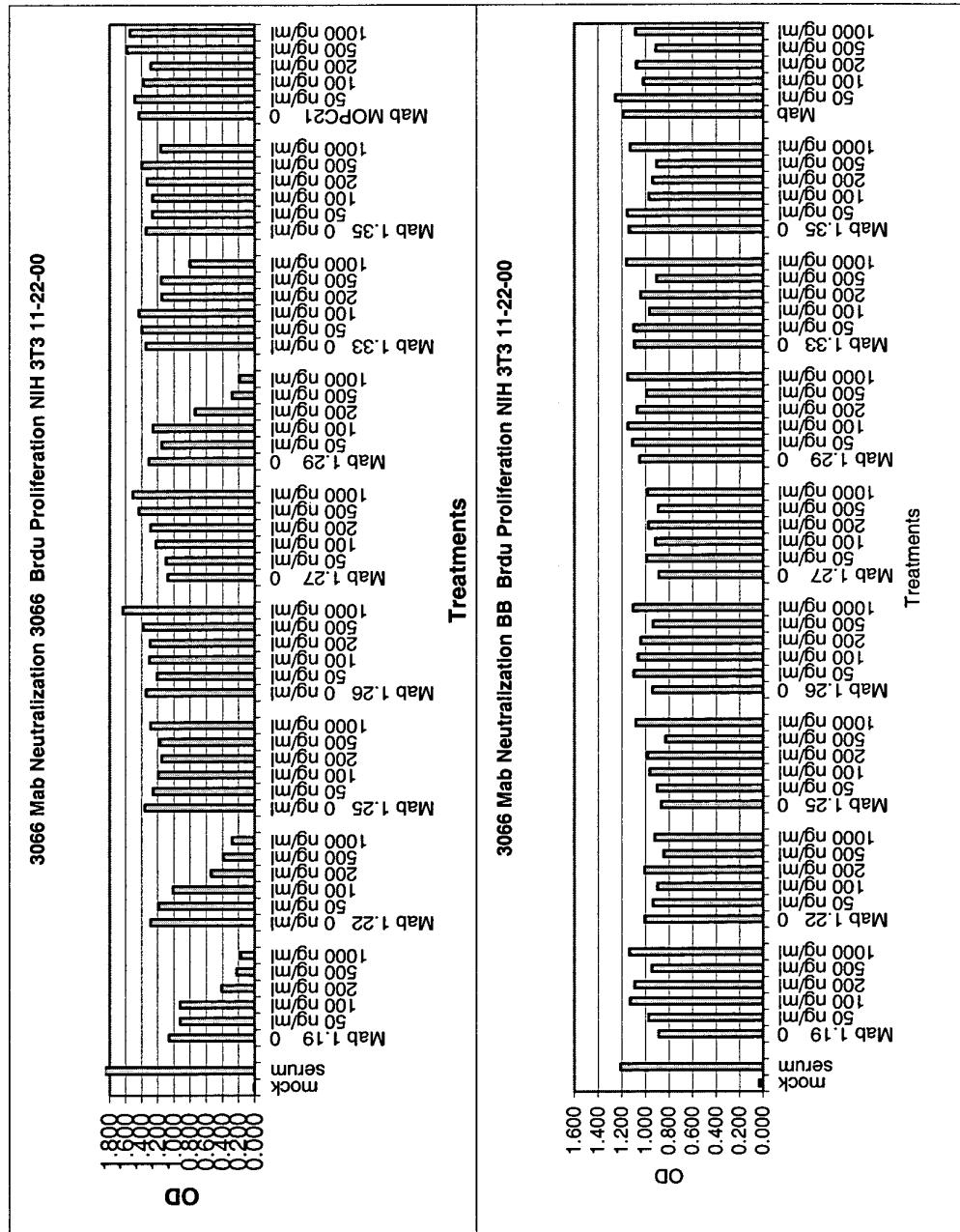
**FIGURE 44**



**FIGURE 45**



**FIGURE 46**



**FIGURE 47**

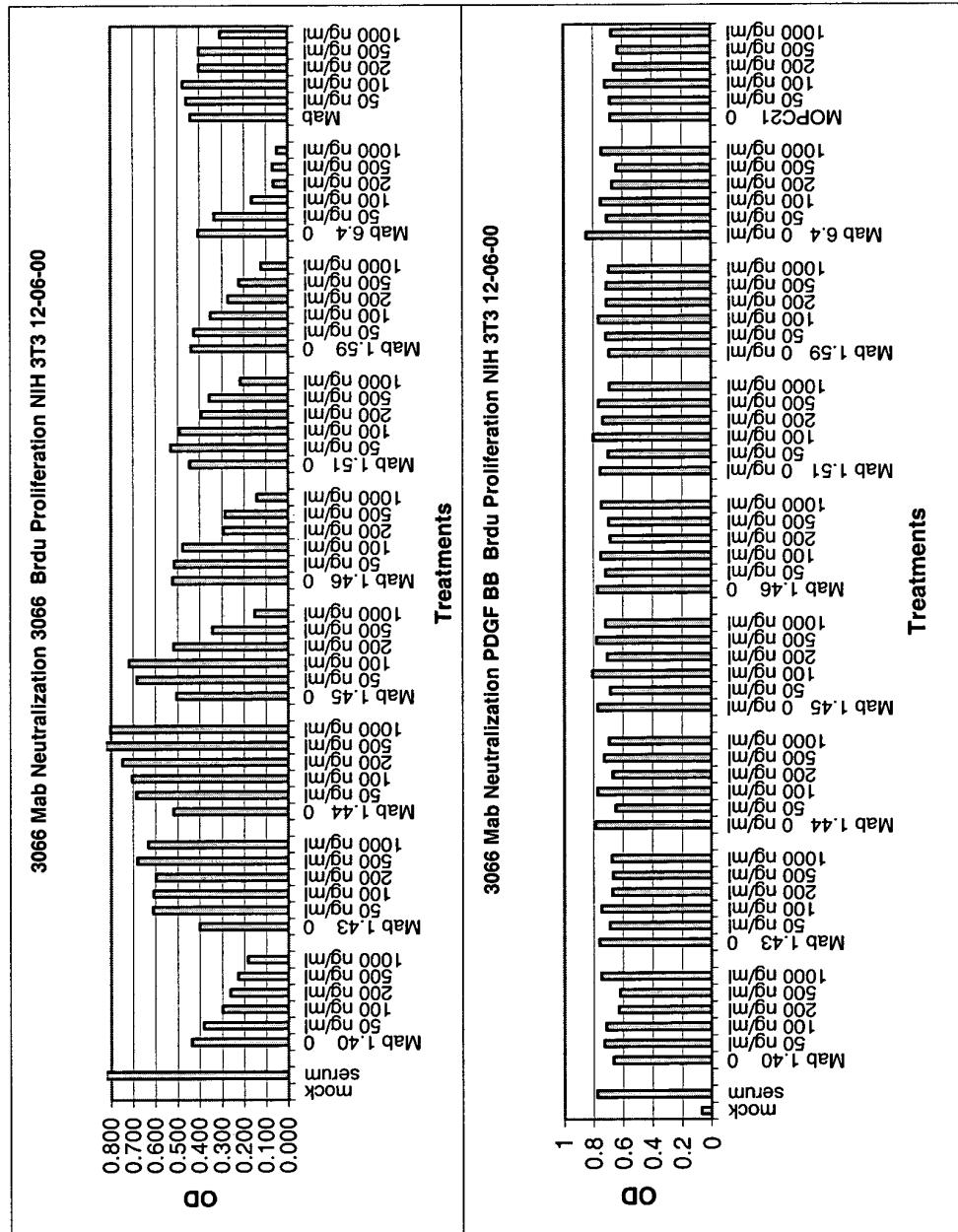


FIGURE 48

|        |   |   | CDR1 | CDR2 |
|--------|---|---|------|------|
| 1.19 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY   |      | 60   |
| 6.4 H  | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTDY   |      | 60   |
| 1.18 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY   |      | 60   |
| 1.40 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY   |      | 60   |
| 1.45 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY   |      | 60   |
| 1.46 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYSFTSYDINWVRQATGQGLEWMGWMNPNNGNTGY   |      | 60   |
| 1.49 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGDTGY   |      | 60   |
| 1.33 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWIISAYNGNTNY  |      | 60   |
| 1.48 H | 1 | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWIISAYNGNTNY  |      | 60   |
| 1.6 H  | 1 | EVQLVESGGGLVQPGGSLRLSCAASGFNFERTYNNWVRQAPGKGLEWVSSISSSSSNIYY  |      | 60   |
| 1.17 H | 1 | QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWAVIIWYDGSNKYY  |      | 60   |
| 1.24 H | 1 | QVQLVESGGGVVQPGRSLRLSCAASGFSPSSYGMHWVRQAPGKGLEWVADIWYDGSNKYY  |      | 60   |
| 1.38 H | 1 | QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWYDGNDKYY  |      | 60   |
| 1.11 H | 1 | EVQLVQSGGGLITQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGS-TYY |      | 59   |
| 1.23 H | 1 | EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIIHYPGDSDTRY |      | 60   |
| 1.25 H | 1 | EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIHYPGDSDTRY |      | 60   |
| 1.29 H | 1 | EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIHYPGDSDTRY |      | 60   |
| 1.39 H | 1 | EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIHYPGDSDTRY |      | 60   |
| 1.51 H | 1 | EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIHYPGDSDAKY |      | 60   |

**FIGURE 48 (CONT)**

|             |          |     |             |     |
|-------------|----------|-----|-------------|-----|
| <b>1.19</b> | <b>H</b> | 117 | GQGTTTVTVSS | 126 |
| <b>6.4</b>  | <b>H</b> | 116 | GQGTTTVTVSS | 125 |
| <b>1.18</b> | <b>H</b> | 117 | GQGTTTVTVSS | 126 |
| <b>1.40</b> | <b>H</b> | 117 | GQGTTTVTVSS | 126 |
| <b>1.45</b> | <b>H</b> | 116 | GQGTTTVTVSS | 125 |
| <b>1.46</b> | <b>H</b> | 117 | GQGTTTVTVSS | 126 |
| <b>1.49</b> | <b>H</b> | 118 | GQGTTTVTVSS | 127 |
| <b>1.33</b> | <b>H</b> | 118 | GQGTTTVTVSS | 127 |
| <b>1.48</b> | <b>H</b> | 116 | GQGTLTVTVSS | 125 |
| <b>1.6</b>  | <b>H</b> | 117 | GQGTLTVTVSS | 126 |
| <b>1.17</b> | <b>H</b> | 117 | GQGTTTVTVSS | 126 |
| <b>1.24</b> | <b>H</b> | 117 | GQGTTTVTVSS | 126 |
| <b>1.38</b> | <b>H</b> | 118 | GQGTTTVTVSS | 127 |
| <b>1.11</b> | <b>H</b> | 111 | GQGTTTVTVSS | 120 |
| <b>1.23</b> | <b>H</b> | 117 | GQGTLTVTVSS | 126 |
| <b>1.25</b> | <b>H</b> | 117 | GQGTLTVTVSS | 126 |
| <b>1.29</b> | <b>H</b> | 120 | GQGTTTVTVSS | 129 |
| <b>1.39</b> | <b>H</b> | 117 | GQGTLTVTVSS | 126 |
| <b>1.51</b> | <b>H</b> | 117 | GQGTLTVTVSS | 126 |

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**FIGURE 49**

|                                 |           |   |
|---------------------------------|-----------|---|
| <b>1.48 L</b>                   | <b>1</b>  | DIQMTQSPSSVSASVGDRVТИTCRASQGISS-----WLA <del>WYQQKPGKAPKLLIYAASTLQ</del> 55   |
| <b>1.49 L</b>                   | <b>1</b>  | DIQMTQSPS <del>L</del> LPVTPGEPAS <del>I</del> SCRSSQS <del>L</del> LHSNGYNYLDWYLLKPGQSPQ <del>L</del> LIYLGS <del>SRA</del> 60   |
| <b>1.11 L</b>                   | <b>1</b>  | DIQMTQSPS <del>L</del> LPVTPGEPAS <del>I</del> SCRSSQS <del>L</del> LHSNGYNYLDWY <del>L</del> KPGQSPQ <del>L</del> LIYLGS <del>NRA</del> 60   |
| <b>1.29 L</b>                   | <b>1</b>  | DIQMTQSPS <del>L</del> LPVTPGEPAS <del>I</del> SCRSSQS <del>L</del> LHSNGYNYLDWY <del>L</del> KPGQSPQ <del>L</del> LIYLGS <del>NRA</del> 60   |
| <b>1.45 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGI <del>N</del> -----DLA <del>WYQQKPGKVPKLLIYAASTLQ</del> 55   |
| <b>1.33 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGI <del>N</del> -----YLA <del>WYQQKPGKVPKLLIYAASTLQ</del> 55   |
| <b>1.38 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGI <del>N</del> -----YLA <del>WYQQKPGKVPNLLIYAASTLQ</del> 55   |
| <b>6.4 L</b>                    | <b>1</b>  | EIVLTQSPGTL <del>S</del> LSPGERATLSCRASQSV <del>SS</del> -----YLA <del>WYQQKPGQAPRLLIYATSSRA</del> 56   |
| <b>1.51 L</b>                   | <b>1</b>  | EIVLTQSPGTL <del>S</del> LSPGERATLSCRASQSV <del>SS</del> -----YLA <del>WYQQKPGQAPRLLIYASNRA</del> 56  |
| <b>1.19 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIYAASSLQ</del> 55   |
| <b>1.18 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIYAASSLQ</del> 55   |
| <b>1.16 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIYAASSLQ</del> 55   |
| <b>1.23 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQTIPGKAPKRLIYAASSLQ</del> 55  |
| <b>1.25 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIYAASSLQ</del> 55   |
| <b>1.39 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIYAASSLQ</del> 55   |
| <b>1.17 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIYAASSLQ</del> 55   |
| <b>1.24 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIYAASSLQ</del> 55   |
| <b>1.46 L</b>                   | <b>1</b>  | DIQMTQSPSSLSASVGDRVТИTCRASQGIRN-----DLG <del>WYQQKPGKAPKRLIFAASSLQ</del> 55   |
| [ <u>CDR1</u> ] [ <u>CDR2</u> ] |           |   |
| <b>1.48 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>D</del> FTLT <del>I</del> SSLQ <del>P</del> EDFASYYCQQSNSF <del>P</del> RT-FGQ <del>G</del> TKVEIK 107  |
| <b>1.49 L</b>                   | <b>61</b> | SGVPDRFSGSGSGT <del>D</del> FTL <del>K</del> IS <del>R</del> VE <del>A</del> EDVG <del>V</del> YYCM <del>Q</del> TLQ <del>T</del> IT--FGQ <del>G</del> TR <del>L</del> EIK 111  |
| <b>1.11 L</b>                   | <b>61</b> | SGVPDRFSGSGSGT <del>D</del> FTL <del>K</del> IS <del>R</del> VE <del>A</del> EDVG <del>V</del> YYCM <del>Q</del> ALQ <del>T</del> LT--FGGG <del>T</del> KVEIK 111   |
| <b>1.29 L</b>                   | <b>61</b> | SGVPDRFSGSGSGT <del>D</del> FTL <del>K</del> IS <del>R</del> VE <del>A</del> DDVG <del>V</del> YYCM <del>Q</del> ALQ <del>S</del> LMCSFG <del>Q</del> GT <del>K</del> LEIK 113  |
| <b>1.45 L</b>                   | <b>56</b> | LGVPSRFSGSGSGT <del>D</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>V</del> ATYYCQ <del>K</del> YNS <del>A</del> P <del>F</del> RT-FGPG <del>T</del> KVD <del>I</del> K 107                                       |
| <b>1.33 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>D</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>V</del> ATYYCQ <del>K</del> YNS <del>A</del> PL <del>T</del> -FGGG <del>T</del> KVEIK 107   |
| <b>1.38 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>D</del> FSLT <del>I</del> SSLQ <del>P</del> ED <del>V</del> AA <del>Y</del> Y <del>C</del> Q <del>K</del> C <del>N</del> S <del>A</del> P <del>W</del> T-FGQ <del>G</del> TT <del>V</del> EIK 107 |
| <b>6.4 L</b>                    | <b>57</b> | TGIPDRFSGSGSGT <del>D</del> FTLT <del>I</del> SR <del>L</del> E <del>P</del> EDFAVYYCQ <del>Q</del> Y <del>G</del> SS <del>P</del> CS-FGQ <del>G</del> TK <del>L</del> EIK 108  |
| <b>1.51 L</b>                   | <b>57</b> | TGIPDRFSGSGSGT <del>D</del> FTLT <del>I</del> SR <del>L</del> E <del>P</del> EDFAVYYCQ <del>Q</del> Y <del>G</del> SS <del>L</del> FT-FGPG <del>T</del> KVD <del>I</del> K 108  |
| <b>1.19 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>D</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> DC <del>P</del> CS-FGQ <del>G</del> TK <del>L</del> EIR 107                          |
| <b>1.18 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> Y <del>P</del> FT-FGPG <del>T</del> KVD <del>I</del> K 107                           |
| <b>1.16 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> Y <del>P</del> FT-FG <del>G</del> GT <del>K</del> VEIK 107                           |
| <b>1.23 L</b>                   | <b>56</b> | RGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> Y <del>P</del> WT-FGQ <del>G</del> TK <del>V</del> EIK 107                           |
| <b>1.25 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> Y <del>P</del> WT-FGQ <del>G</del> TK <del>V</del> EIK 107                           |
| <b>1.39 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> Y <del>P</del> WT-FGQ <del>G</del> TK <del>V</del> EIK 107                           |
| <b>1.17 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> Y <del>P</del> WT-FG <del>G</del> GT <del>K</del> VEIK 107                           |
| <b>1.24 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> N <del>S</del> Y <del>P</del> WT-FGQ <del>G</del> TK <del>V</del> EIK 107                           |
| <b>1.46 L</b>                   | <b>56</b> | SGVPSRFSGSGSGT <del>E</del> FTLT <del>I</del> SSLQ <del>P</del> ED <del>F</del> ATYYC <del>L</del> Q <del>H</del> S <del>G</del> Y <del>P</del> FT-FGQ <del>G</del> TK <del>V</del> EIK 107                           |
| [ ] [ <u>CDR3</u> ]             |           |   |

**FIGURE 50**

|               |   |   |    |
|---------------|---|---|----|
| <b>1.19 H</b> | 1 | QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY               | 60 |
| <b>6.4 H</b>  | 1 | QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGW <del>W</del> NPNSGNTDY  | 60 |
| <b>1.18 H</b> | 1 | QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY               | 60 |
| <b>1.40 H</b> | 1 | QVQLVQSGAEVKPGASVKVSCKASGYTFT <del>T</del> SYDINWVRQATGQGLEWMGWMNPNSGNTGY | 60 |
| <b>1.45 H</b> | 1 | QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY               | 60 |
| <b>1.46 H</b> | 1 | QVQLVQSGAEVKPGASVKVSCKASGY <del>S</del> FTSYDINWVRQATGQGLEWMGWMNPNNGNTGY  | 60 |
| <b>1.49 H</b> | 1 | QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSG <del>E</del> TGY  | 60 |

[ CDR1 ]

[ CDR2 ]

|               |    |   |     |
|---------------|----|---|-----|
| <b>1.19 H</b> | 61 | AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGG-VIV <del>HY</del> GMDVWGQG             | 119 |
| <b>6.4 H</b>  | 61 | AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYC <del>V</del> RGFGYSYN--YDYYYGMDVWGQG             | 118 |
| <b>1.18 H</b> | 61 | AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGT-YYYYYYGMDVWGQG                         | 119 |
| <b>1.40 H</b> | 61 | AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVAA-TNYY <del>N</del> GMDVWGQG             | 119 |
| <b>1.45 H</b> | 61 | AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG--YDYYYGMDVWGQG                          | 118 |
| <b>1.46 H</b> | 61 | AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVTA-TDYYYGMDVWGQG                          | 119 |
| <b>1.49 H</b> | 61 | AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVY <del>E</del> CARMRDIVATSYYY <del>Y</del> YGMDVWGQG | 120 |

[ CDR3 ]

[ CDR3 ]

|               |     |         |     |
|---------------|-----|---------|-----|
| <b>1.19 H</b> | 120 | TTVTVSS | 126 |
| <b>6.4 H</b>  | 119 | TTVTVSS | 125 |
| <b>1.18 H</b> | 120 | TTVTVSS | 126 |
| <b>1.40 H</b> | 120 | TTVTVSS | 126 |
| <b>1.45 H</b> | 119 | TTVTVSS | 125 |
| <b>1.46 H</b> | 120 | TTVTVSS | 126 |
| <b>1.49 H</b> | 121 | TTVTVSS | 127 |

**FIGURE 51**

**1.33 H 1** QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60  
**1.48 H 1** QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60  
[ CDR1 ] [ CDR2 ]

**1.33 H 61** AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--DHYYDSSSDYLYYYGLDVWG 118  
**1.48 H 61** AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYDGSYYYEDY---WG 116  
[ CDR3 ]

**1.33 H 119** QGTTVTVSS 127  
**1.48 H 117** QGTLVTVSS 125

**FIGURE 52**

|                   |  |                              |     |
|-------------------|--|------------------------------|-----|
| <b>1.17 H 1</b>   | QVQLVESGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDG | <b>SNKYY</b>                 | 60  |
| <b>1.24 H 1</b>   | QVQLVESGGVVQPGKSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIWYDG | <b>SNKYY</b>                 | 60  |
| <b>1.38 H 1</b>   | QVQLVESGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWYDG | <b>NDKYY</b>                 | 60  |
|                   | [ <u>CDR1</u> ]  | [ <u>CDR2</u> ]              |     |
| <br>              |  |                              |     |
| <b>1.17 H 61</b>  | ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY-RYAGY       | <b>YYDYGMDVWGQG</b>          | 119 |
| <b>1.24 H 61</b>  | ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY-SYGY        | <b>VYYDYGMDVWGQG</b>         | 119 |
| <b>1.38 H 61</b>  | ADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARG                | <b>YYDSSDYLYYYYYGMDVWGQG</b> | 120 |
|                   | [ <u>CDR3</u> ]  |                              |     |
| <br>              |  |                              |     |
| <b>1.17 H 120</b> | TTVTVSS  | 126                          |     |
| <b>1.24 H 120</b> | TTVTVSS  | 126                          |     |
| <b>1.38 H 121</b> | TTVTVSS  | 127                          |     |

**FIGURE 53**

|             |          |   |   |    |
|-------------|----------|---|---|----|
| <b>1.23</b> | <b>H</b> | 1 | EVQLVQSGAEVKKPGESLKISCKGSYRFTSYWIGWVRQMPGKLEWMGIYPGDS | 60 |
| <b>1.25</b> | <b>H</b> | 1 | EVQLVQSGAEVKKPGESLKISCKGSYRFTSYWIGWVRQMPGKLEWMGIYPGDS | 60 |
| <b>1.29</b> | <b>H</b> | 1 | EVQLVQSGAEVKKPGESLKISCKGSYRFTSYWIGWVRQMPGKLEWMGIYPGDS | 60 |
| <b>1.39</b> | <b>H</b> | 1 | EVQLVQSGAEVKKPGESLKISCKGSYRFTSYWIGWVRQMPGKLEWMGIYPGDS | 60 |
| <b>1.51</b> | <b>H</b> | 1 | EVQLVQSGAEVKKPGESLKISCKGSYRFTSYWIGWVRQMPGKLEWMGIYPGDS | 60 |

[\_\_CDR1\_\_] [\_\_CDR2\_\_]

|             |          |    |   |     |
|-------------|----------|----|---|-----|
| <b>1.23</b> | <b>H</b> | 61 | SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCYCARHVSY <del>YYVSG</del> ---SYNNVFDYWG              | 117 |
| <b>1.25</b> | <b>H</b> | 61 | SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCYCARHGS <del>YYGSE</del> ---TYYNVFDYWG               | 117 |
| <b>1.29</b> | <b>H</b> | 61 | SPSFQGQ <del>A</del> TISADKSISTAYLQWSSLKASDTAMYCYCARHV <del>DVGATIG</del> YYYYYYHGMDVWG | 120 |
| <b>1.39</b> | <b>H</b> | 61 | SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCYCARHGS <del>YYNSG</del> ---SYNNVFDYWG               | 117 |
| <b>1.51</b> | <b>H</b> | 61 | SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCYCARHY <del>DYVWRNY</del> ---RYTGWFDPWG              | 117 |

\_\_\_\_\_] \_\_\_\_\_] CDR3 \_\_\_\_\_]

|             |          |     |            |     |
|-------------|----------|-----|------------|-----|
| <b>1.23</b> | <b>H</b> | 118 | QGTLTVTVSS | 126 |
| <b>1.25</b> | <b>H</b> | 118 | QGTLTVTVSS | 126 |
| <b>1.29</b> | <b>H</b> | 121 | QGTTTVTVSS | 129 |
| <b>1.39</b> | <b>H</b> | 118 | QGTLTVTVSS | 126 |
| <b>1.51</b> | <b>H</b> | 118 | QGTLTVTVSS | 126 |

and the  $\text{H}_2\text{O}_2$  was added to the reaction mixture.

**FIGURE 54**

**1.49 L 1** DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLLKPGQSPQLLIYLGS SRA 60  
**1.11 L 1** DIVMTQSPLSLPVTPGEPASISCRSSQSLLQSNGNYLDWYLLQKPGQSPQLLIYLGS NRA 60  
**1.29 L 1** DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLLQKPGQSPQLLIYLGS NRA 60  
[  CDR1  ] [  CDR2  ]

**1.49 L 61** SGVPDRFSGSGSGTDFTLKISRVEAE DVGVYYCMQTLQTLT--FGQGTRLEIK 111  
**1.11 L 61** SGVPDRFSGSGSGTDFTLKISRVEAE DVGVYYCMQALQTLT--FGGGTKVEIK 111  
**1.29 L 61** SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLIMCSFGQGKLEIK 113  
[  CDR3  ]

**FIGURE 55**

**1.45 L** 1 DIQMTQSPSSLSASVGDRVTI**NCRASQG**I**SN**DLAWYQQKPGKVPK**L**LIYA**AS**T**Q**LG**V**P**S** 60  
**1.33 L** 1 DIQMTQSPSSLSASVGDRVTI**T**CRASQG**I****SN**YLA**W**YQQKPGKVPK**L**LIYA**AS**T**Q**SG**V**P**S** 60  
**1.38 L** 1 DIQMTQSPSSLSASVGDRVTI**T**CRASQG**I****SN**YLA**W**YQQKPGKVP**N**LIYA**AS**T**Q**SG**V**P**S** 60  
[ CDR1 ] [ CDR2 ]

**1.45 L** 61 RFSGSGSGTD**F**LT**T**LISS**L**Q**P**ED**V**A**T**YY**C**Q**K**Y**N**SA**F**TF**G**F**G**T**K**V**D**I**K** 107  
**1.33 L** 61 RFSGSGSGTD**F**LT**T**LISS**L**Q**P**ED**V**A**T**YY**C**Q**K**Y**N**SA**E**LT**F**GG**G**T**K**V**E**I**K** 107  
**1.38 L** 61 RFSGSGSGTD**F**SL**T**LISS**L**Q**P**ED**V**A**A**YY**C**Q**K**C**N**SA**P**WT**F**G**Q**GT**T**V**E**I**K** 107  
[ CDR3 ]

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**FIGURE 56**

**6.4 L** 1 EIVLTQSPGTLSSLPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSSRATGIP 60  
**1.51 L** 1 EIVLTQSPGTLSSLPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASN RATGIP 60  
[ CDR1 ] [ CDR2 ]

**6.4 L** 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQG GTKLEIK 108  
**1.51 L** 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK 108  
[ CDR3 ]

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**FIGURE 57**

|               |   |   |    |
|---------------|---|---|----|
| <b>1.19 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.18 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.16 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWFQQKPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.23 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQTPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.25 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.39 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.17 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.24 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS | 60 |
| <b>1.46 L</b> | 1 | DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS | 60 |

[ CDR1 ] [ CDR2 ]

|             |          |    |   |     |
|-------------|----------|----|---|-----|
| <b>1.19</b> | <b>L</b> | 61 | RFSGSGSGTDFLTISLQPEDFATYYCLQHNSDPCSFQGTKLEIR    | 107 |
| <b>1.18</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYFCQLQHNSYPFTFGPGTKVDIK | 107 |
| <b>1.16</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKVEIK  | 107 |
| <b>1.23</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGTKVEIK   | 107 |
| <b>1.25</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGTKVEIK   | 107 |
| <b>1.39</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGTKVEIK   | 107 |
| <b>1.17</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKVEIK  | 107 |
| <b>1.24</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGTKVEIK   | 107 |
| <b>1.46</b> | <b>L</b> | 61 | RFSGSGSGTEFTLTISLQPEDFATYYCLQHSGYEPPTFGQGTKVEIK | 107 |

[ CDR3 ]